

APPENDIX A: DNA SEQUENCES

>RXA00001-upstream

TGTCATAGGCAGCACTCTAGATGGCGCACAGTGAAGTCACTTCACTGTTTCTCACACTACG
GATCGTTTCGGCACGTACCTGCCGATGGAGGAGATTCTGCA

>RXA00001

ATGGCAACCGTAACGTTCAAAGATGCTTCCCTAAGCTACCCGGGAGCAAAGGAACCCACC
GTCAAGAAATTCAACCTGGAAATCGCCGATGGCGAGTTCTCGTCTCGTCGGCCCTTCC
GGCTGTGGTAAATCCACCACGCTGCGCATGCTGGCCGTTTGGAAAACGTTACTGACGGT
GCCATTTTTCATCGGAGACAAGGACGTTACCCACGTTGCACCGCGTGACCGTGACATCGCC
ATGGTTTTCCAGAACTATGCTCTCTACCCCCACATGACCGTGGGCGAGAACATGGGCTTC
GCACTGAAGATCGCCGGCAAGTCCCAAGACGAGATCAATAAGCGCGTCGACGAAGCCGCC
GCCACTTTGGGCTGACCGAATTCTTGGAGCGCAAGCCGAAGGCCCTGTCCGGTGGTCAG
CGTCAGCGTGTGGCCATGGGCGCGCCATTGTTGCAACCCGACAGTCTTCTCATGGAT
GAGCCGCTGTCTAACCTCGATGCCAAGCTGCGTGTTCAGACCCGTACCCAGATTGCAGCC
CTGCAGCGCAAGCTTGGGGTTACCACCGTTTACGTACCCACGACCAGACGAGGCCCTTG
ACCATGGGTGACCGCATCGCGGTGCTGAAGGATGGCTACCTGCAGCAGGTTGGCGCGCCC
CGAGAGCTTTATGACCGCCCCGCAACGCTCTCGTCGCGGCTTCATCGGCTCCCCAGCC
ATGAACCTGGGCACCTTCTCGGTCAAGGATGGTGACGCTACCTCTGGTCACGCTCGCATC
AAGCTTTCCCGGAAACCCCTCGCCGCCATGACGCCGAGGATAATGGCCGCATCACCAT
GGTTTCCCGCCGAGGCACTGGAGATCATTCCGGAAGGCGAGTCCACCGATCTTTCCATC
CCAATCAAGCTCGACTTCGTGGAGGAACCTCGGTTCCGATTCTTCTCTACGGCAAGCTG
GTAGGCGAGGGCGACCTTGGATCCTCCAGCGAGGATGTCCCGAGTCCGGCCAAATCGTC
GTCCGCGCTGCTCCGAACGCCGCGCTGCTCCGGGACAGTGTTCACGACGCATCGTG
GAGGGCGGCCAGCACAACTTCTCGGCGTCGACTGCAAGCGCCTCCCT

>RXA00001-downstream

TAAGCCCGCGTACCGGCTACCCC

>RXA00002-upstream

CTGACTTCTTGGGCTTCGGTGCTGCAATATCTAGGTTACGCCCCGGATGGCACCGGAGA
GGCTGCAGACAAGCTCGCTGCTGAGGATTCTCACCTGCAC

>RXA00002

GTGCTGCACCGCGAAGGCAAGGGTGGCCTTCTTGGCGCTTATATCGCCGGCTTCGAGTGG
GGCCTAGAGAAGGATTACCATGTTCTGTGCGAAATGGATGCGACGGCTCCACGCACCA
GAACAGCTCCACCTCTTGCTTGAGGAAATTGAAAAGGGCGCAGATCTGGTCATTGGCTCC
CGCTACGTACCGGGTGGAGAGACAGTGAACCTGGCCTGCCAACCGCGAACTGCTGTCCCGC
TTGGGCAACAAGTACATTTCTGTTGCCCTGGGTGCCGGCATCAATGACATGACTGCCGGC
TACCGTGCTTTCCGGCGTGAGCTGCTTGAGCACCTCGACTTTGAGGAGCTTTCCAACGCC
GGATACATCTTCCAGGTGGACGTTGCCTTCCGCGCCATCAAGGATGGCTTCGATGTCCGC
GAGGTTCCGATCACCTTACCGAGCGCAGCTTGGTGAATCCAAGCTGGACGGCTCCTTT
GTCAAGGATTCCCTGCTCGAAGTAACCAAGTGGGGAGTGGCTCACCGCTCCGAGCAGATC
AGCGATTTACATCGGAAGTATCCAAGATCGCCTCCCGCACGGTCAAGGACATGGAGCTT
GGCCCTAAGGCCACCACGGCCAAGAAGCTGTACCGGACTTCGTTTCCGAAGTCTCTAAC
CTAGCTAAAGGCACCTTCAAGAAG

>RXA00002-downstream

TAACTCGATGCCCCGCGCGTCTC

>RXA00089-upstream

ACCTCGTTTTGGCCGCAAGTTCTCGTTAGTTAAAACTGTAGGAAACCAGGTTCCACACA
TGACACACAATCGGTTTAAACAGGGAAGGGGATCGGCACTG

>RXA00089

ATGGCAACACCAGCATCGGCTCCCACTTCCGAACCACGTCTCAAACGCACCAGAGCCAA
CTTTTTGATTGGAAGCTTCTCATCGGCATCATTTTCGTGCGCCGGCCTCGTGGTGCTTTCC
CTCCTCACCGGCCAATACGACATTTTCGGTGGCGATGATGGCCAACCTGATGTTCGAGGCA
GTTTCGATCCCGCGTACCGTTTCCCTCATTTTGTCCGGTGCAGCAATGGCGATGTGTGGC

TTAGTCATGCAGCTGTTGACCCAAAACAAATTCGTGGAACCCAGCACCACAGGAACAACC
 GAATGGGCAGGTCTTGGCCTCCTCTTCGTGATTTACTTCGTGCCAGCCGCGACCGTTTGG
 GATCGCATGCTCGGTGCCGTGGTGTTCCTTCATCGGAACCATGGTGTCTTCCTCTTT
 CTACGCCGAGTAACACTGCGTTTCTCATTGATCGTCCCGATTATCGGCATCATGCTCGGT
 GCCGTGGTGTATCGATCTCCAGCTTCTTCGCCTTGCAATTCGACATGCTCCAGCAATTG
 GGAACATGGTTTGGGGTTCCTTTAATACAGTGTTCCGCGGACAGTACGAAGTGCTGTGG
 ATCGTTGTATCGTCGTTATTGCAGTGTTCTTCTTCGCAGACCGGCTCACCGTAGCTGGC
 CTTGGCGAGGAAATCGCGACAAACGTGGGTCTCAATTACAACCGCATGGTCTTATCGGA
 ACTGGCCTCATCGCCATCGCAACAGGTGTGGTCAACCGTCGTGGTGGTAGCCTGCCATT
 CTCGGACTCATCGTGCCCAACGTTGTGTCCATGTTCCGTGGCGATGACCTGCGCTCGAAC
 CTGCCATGGGTATGCCTAACCGGCATCGCGATCGTAACCATTGTGACTTGATCAGCCGA
 ACCATCATCGCGCCTTTCGAAATTCCAGTTTCAGTAATCCTGGGCATCATCGGCGCAGTG
 GTCTTCGTGATCATGATTGTGAGGCAACGTGGCCGTGGA

>RXA00089-downstream
 TAAAGATATTGAAAACCGCACCT

>RXA00090-upstream
 TTGATCAGCCGAACCATCATCGCGCCTTTCGAAATTCCAGTTTCAGTAATCCTGGGCATC
 ATCGGCGCAGTGGTCTTCGTGATCATGATTGTGAGGCAAC

>RXA00090
 GTGGCCGTGGATAAAGATATTGAAAACCGCACCTCAGACCTTTCTCGATGGGAAACTATG
 GAGGAATCAGCAACGGTCGAGGGACGCACCGATGTGCAACTAGCATCAGCGCCGAGCAAA
 CGACGCACCTCAGGTGCATTCCAAACAGCGCGCGCCAAGCGCCGCTACTGGATCATCATG
 GCGCGCTGCTGGTCACCGCCTTGCCTTCACCTGGGGCCTCATTGGGTACAAGAACCCG
 ATGCCCGTTGGGCATCCGGCCTTCGCGCTGATTGCAGAACGACGCATGGAGTCGGTCTTT
 GTCATGCTGATTGTTGCGGTTTGCCAAGGCTTTGCGACGGTTGCGTTCAGACCGTCACC
 AACAACCGCATTATCACGCCGTGATCATGGGCTTTGAATCTCTCTACACACTGATTCAT
 ACCTCCACAGTGTTCTTCTTCGGCGCAACTGCACTGCTGGCCACCAGAAATCTCGAAATG
 TTTGTGCGCCAGCTGGTGATCATGGTCTTTTGACCTTGGTCTCTACACCTGGCTGCTT
 TCCGGAACCGCGCGATATGCACGCCATGCTGCTTGTGCGCATCATCATTGGTGGCGGA
 CTCGGATCCATCTCCACCTTATGCAGCGCATTCTGACCCCATCAGAATTGATATTCTT
 TCCGCCGACTTTTCGGATCAGTAACAACCGGAAACCGAATACTTCCCAATTGCTGT
 CCACCTAGTAGTAGTGGCGTCCGTCTTGTGCTGCTAAGCTCTCGACGCCTCAACGTTGTA
 GGGCTTGCAAGATGCCGCAACCAACCTTGAATTAATCACCGACGATCCTCCATTTAC
 ACCTGGTCTCTGCTCTGTATTAATGGCAGTATCCACCGCACTTGTGCGACCGATGACA
 TTCTTCGGATTCTTGGTCGCGACCTTGGCATATCAATTGCGCGACACTTACGACCACCGA
 TACATCCTTCCGATGTCCGCACTCATCGGATTGCTCGTACTCAGCGGCGCTTACTTTGTC
 ATGAACCACGTGTTCCGCGCACAAGGCGTCTGTGTCATCATTATTGAGATGGTCCGGCGGT
 ACCGTCTTCCTCATCGTCATCCTCAGAAAGGGCAGACTG

>RXA00090-downstream
 TGATTACGTTAACTAATGTCCGC

>RXA00099-upstream
 CTCTGGTGAAGAGGATGTTGACTCGGGAGATTCTTCCACTGATTCACTGATTAAGTGGTA
 CCGCGCAAATAGGTAGTCGCTTGCTTATAGGGTCAGGGGC

>RXA00099
 GTGAAGAATCCTCGCCTCATAGCACTGGCCGCTATCATCCTGACCTCGTTCAATCTGCGA
 ACAGCTATTACTGCTTTAGCTCCGCTGGTTTCTGAGATTCGGGATGATTTAGGGGTTAGT
 GCTTCTCTTATTGGTGTGTTGGGCATGATCCCGACTGCTATGTTGCGGGATGCTGCGTTT
 GCGCTTCCGTGCTTGAAGAGGAAGTTCACTACTTCCCAACTGTTGATGTTTGCCATGCTG
 TTGACTGCTGCCGGTCAGATTATTCGTGTCGCTGGACCTGCTTCGCTGTTGATGGTCCGT
 ACTGTGTTGCGGATGTTTGGCATCGGAGTTACCAATGTGTTGCTTCCGATTGCTGTTAGG
 GAGTATTTTCCGCGTCACGTCCGTGGAATGTCGACAACCTTATCTGGTGTGCTTCCAGATT
 GTTCAGGCACTTGCTCCGACGCTTCCGCTGCCGATTCTCAGTGGGCTACACATGTGGGG
 TTGACCGGTTGGAGGTGTGCTCGGTTGCTGGGCGCTGCTGGGGTTGGTTGCGGCGATT
 TCGTGGATTCCGCTGTTGAGTTTGCAGGGTGCCAGGGTTGTTGCGGCGCCGTCGAAGGTT
 TCTCTTCCTGTGTGAAGTCTTCGGTTGGTGTGGGGCTCGGGTTGATGTTTGGGTTTACT

TCGTTTGGCGACGTATATCCTCATGGGTTTTATGCCGCGAGATGGTAGGTGATCCTCAGCTC
 GGTGCGGTGTTGTTAGGCTGGTGGTCAATTTTGGGATTGCCGCTGAACATTCTGGGACCG
 TGGTTGGTGACGCGTTTCACTAACTGCTTCCCGATGGTTGTTATCGCCAGTGTGATGTTT
 CTCATCGGTAATGGTGGGTTTTGTTTGGCTCCGGATGTTGCGCCGTGGTTGTGGGCGACG
 TTGTCTGGTCTTGGTCCCTTGGCTTCCCGATGGCGTTGACGCTCATTAATATTCTGCTGCT
 GAAACTAGTGTCTGGTGTCTTCTGCGTTGAGTTCCTTCGGGCAGGGTTTGGGTTATACGATT
 GCGTGTTCGGTCCCTTGTGACTGGTTTCATTGTGCGATGCAACAGGCAGCTTCCGAACA
 ATCTTTTTGCTTTTTTGGGGTGCAACACTCTTCGTTATTAGAGGCGGTACTTTGCGACA
 AGGCAGGTTTACGTGCAAAAGCTTTTAAATCGC

>RXA00099-downstream
 TAGGATGGCGCTATGCCGCAAAG

>RXA00123-upstream
 GAAGGATCGTCAGAATAGCTCTCGAATAGGCCATTTCTTACTTCATCGGCAATACTGACT
 TAGTAGAAATTGCTGTCCAGAAGTGTGAAGGAGTTGAAA

>RXA00123
 ATGCCAAAGAATTACGACATCAACGGGGCGATCCGCGAGACGGGATATGCTCAGACGTCGG
 TACCTTCCTGATTTCGGCAAATTCAACTCCTGTACCTGAAGAGGTTTCTCCGCTGACCCGC
 TATGTCACCGACGGCATCCCGAAGCGCCACCGCTGGGTGCCACTGTTGCTGACGGTTTTA
 AAATTCGCCGAAGGCGCCTCCAACCGCATGGTCATGTCGCTGTACCCTGCGCCATCCAAG
 CCCGCAATCGAGGAATTGGCAGAGGCCTGGGACCTCCACCCACCATCGTAGAAGACTTG
 CTCCTTGGTCAGCAGCGCCCAAACTAGACCGCTACGAAGACATCATTTTTATCGCGATC
 CGCTCCGCGCGCTACATCGACTCCCGCGAAGAGGTGGACTTCTCCGAATTCACATCCTC
 ATGAAGCCTCAGGCCATAGCCATTTTGTGCCAGGATAACCAATGGATTGACGGCACCAGC
 GCCGCCAGCTTCAGCAACCCCGAGGAGATCGATAAGCGCATAAAAAACATTGCTTGCCGAC
 GCCGAGTTACTCTCGTCCGGCCCCCGCGCGCGGCTATAGGCTTCTCGACGCCATCGTC
 GACGGCTTCTCCCCCGTTCTTAGAGGCATCGCCATCGACCAGGAACAGATTGAGCGCCAG
 GTGTTCTCCGGCGACGCCCGCGTCGCCGAACGTATTTACAACCTGTCCCAAGAAATCATC
 GACATGCAGCACACCACAGCTCAGTTACCGAAGTGGTGCAACGCCTCAACAAAGACTTC
 ATCCGAAGTGGCATGTCCGAAGAACTCCGCGCCTACCTCGACGACGTCCGCCACCACCTC
 ACCCGCGACAACACCCGCGTCTCCGAATACCGCGAATCCCTATCCCAAATTTTGAACGTC
 AACGCCACCCTTGTAGCCCAACGCCAAACGCAAGACATGAAGAAAATCTCCGGATGGGCC
 GCCATCATCTTCGCCCCAACCCCTCGTGTCTCCATCTACGGCATGAACCTCGACATCATG
 CCAGAATTCACTGGGCGTTTGGCTACCCGTTGGCTCTCTTAGCAATGCTCGGATTACCC
 CTCCTTTTGTACTGGATCTTCAAACGCAGTAAGTGGATG

>RXA00123-downstream
 TGAGACAAAACCGAAAAACCAA

>RXA00160-upstream
 TACAGGGGTGGGGTTACCCCTAAGGTGGTCACAACCTTGATAACGGACTGGTTAATAAAT
 GGCCAATCTGACCATTTTAACCTCCATAAAAAGGATTCTC

>RXA00160
 ATGCTAAACATCGCACGCAACCGCAACATGAAGCGTCGACTAGCAATTGCTGCTTTTCGTC
 GCCACCGCAACCGCTACCGCCACCATGGCACCAGCATCCGCGCAAACCGACTACGCAGGC
 CTTTCCTCCGGCGTTGCCGACACCGTCGCAGAAGCTGCAGGAGTCGCAACCACCGCCGTC
 GCACCAGCCCGCCACCGTAGCGCGCCAGCAAACGGCACCTTCACCTCAGGATTCCGGACCA
 CGTTGGGGAACTTCCACAACGGCATCGACATCGCAAACCTCAATCGGCACCCCAATCTAC
 GCCGTGATGGCCGGCACTGTCATCAGCTCTGGCCCAGCATCCGGCTATGGACAGTGGATC
 CGCATCCAGCACGACGACGGATCCATCTCCATCTACGGACACATGGAATACCTCTACGTC
 TCCGTCCGGCGAACGCGTCGCAGCAGGCCAGGAAATCGCAGGAATGGGCAGCCAAGGATTC
 TCCACCGGCTCCACCTCCACTTCGAGATCCACCCAGACGGCGTCACCCAGTCGACCCA
 CAGGCATGGCTCGCAAACACGGCATCTACGTT

>RXA00160-downstream
 TAAGCGCTAGCCGTTCTGTTGGAT

>RXA00193-upstream
CCTCAGCCTCCTCTCCTCACCGCCTTCCCCGCTGGGAAACGTGTGGCACCACCTGAAATT
AAGGTTTACCACC

>RXA00193
ATGCAAGCAACGCTGAAGAAGTACTTCCCAGTCTTTGTCTTGCCCAACCCTTCTGGCATTCT
ATGATTGCCTTCTTGGTGCCGTTTCATCGTGGGTTTCTTCCCTCTCCTTTACGAAGTTTACC
ACTATCACCAACGCCAAGTGGGTTGGCATAGACAACACTACGTCAAAGCTTTCTCCCAACGC
GAAGGTTTCATCTCAGCCTTCGGTTTACCGTCTCGTGGTCATCGTCTCCGTGATCACA
GTCAACATCTTCGCCCTTCTCTTGGCGTGTTGCTGACCCGCAAACCTCCGCGGTACCAAC
TTTTTCCGCACAGTCTTCTTTATGCCGAACCTTATCGCGCGCATTTGTGCTGGGTTATACC
TGGCAGACCATGATCAACGCCGTGCTTTCGCACTATGCCACGACTATTAGCGCGGACTGG
AAATTCGGCTACGCCGGCCTCATCATGCTACTTAACTGGCAGCTCATCGGCTACATGATG
ATCATTTACATCGCCGGCCTGCAAACGTCCCACCAGAGCTCATTGAGGCTGCCGAACCTC
GACGGCGTCAACAAGTGGGAGATGCTGCGGCACGTCACTATTCCGATGGTTCATGCCATCC
ATCACCATCTGCCTCTTTTGGACTTTGTGCAACTCCTTTAAGCTCTTCGACCAGAACCTG
GCGCTGACCAACGGCGCTCCTGGCGGGCAAACCTGAGATGGTGGCGCTCAACATCATCAAC
ACGCTGTTTAAACCGTATGAATGTCGAGGGCGTCGGTCAGGCCAAGGCCGTTATCTTCGTC
GTCGTTGTGGTTCGTCATCGCTACTTCCAGCTGCGCGGACCCGCTCCAAGGAAATCGAG
GCT

>RXA00193-downstream
TAAGTTATGACTACCAGCACTTC

>RXA00203-upstream
AGGAAGCTGCTGCAGAAATCGAAAACACAAAGGAGGACCGTTGAGCACCGCCGTAGTTTC
ACAGAAGAAGTCCACAACGGCATCCAAATTGGACATTGG

>RXA00203
ATGCTCAATAACGGTGCGTTGGTGGGGCTGATTGCACTGTGTGTTGGACTTTTTATTGCA
ACACCCCACTTTCTCACCATTCCTAACCTGATCAACATCGGTATCCAATCGGCGACGGTG
GCGATCCTGGCGTTCCGGCATGACCTTCGTTCATCGTTACCGCAGGCATTGATTTGTCTGTG
GGATCAGTGGCTGCGTTGGGTGCGATGACCTCGGCGTATTTCTTCGCGGAAGTTGGTTTG
CCGGGCTGGATCAGCTGCTGATTGGCCTGTTTCATCGGATTGTTGGCGGGTGCGATCTCT
GGCATTCTTATTGCTTATGGCAAGTTGCCTGCGTTTATTGCCACCTTGGCCATGATGTGCG
ATCGCCAGGGGAATCACCTTGGTCATTTCCCAAGGCTCACCAATTCCCAGTGCACCAGCT
GTGAACGCTTTGGGGCGCACCTACTTTGGCATCCCGATGCCGATTCTGATGATGGCACTG
GCTGGCATTTGTGTGTTGGTTTATTTTGGAGCCGCACCGTGCTGGGACGGTCCATGTACGCC
ATTGGCGGAAACATGGAAGCAGCCCGACTATCTGGTCTGCCAGTGAAGAAAATCCTGGTC
ATGGTCTATGCACTGGCTGGTGTGTATGCAGCACTTGCGGGTCTGGTCATGACGGGACGC
TTGTCGTCCGCGACGCCGAGGCAGGCGTGGGATACGAACCTGATGCGATTGGCGCCGTG
GTGATGTTGGTGGTGCGTCACTTGTGCGGGAACCGGAAAGCAACGGGCACTTTGATTGGT
GCCATCTTGTGGCCGTGATCCGCAATGGCTTGAACATTTTGAACGTGTCCTCGTTCTGG
CAGCAGATTGTTCATCGGTTGTGTTCATCGCGCTTGCGGTGGGCTTCGATGTTCATCCGAAAC
AAAACCTCTAAG

>RXA00203-downstream
TAATTCCTGAAAGGAAATTTTCA

>RXA00204-upstream
TCAACGGCGGTTTCCCAAAGGCGGCCGCAAAGGCAGCAAAGCAGCCCAAAAAGCAGCC
GCGAAAGCCGCACAGAACACGCAACACGAGGTGAGCCTAG

>RXA00204
ATGGTGAACCTCTGAACAAGCGCTTCATCAGCATGATCCTGCACCAATCCTTCAGTTGGAT
AAAGTCTCCAAGTCGTTTGGCCCACTCAACGTCAATTAATCAAGTGAGCATCGATGTTTCG
CCTGGCAGGTGCTTGGCGTGTGGGTGAAAATGGTGCGGGTAAATCTACGCTGATCAAG
ATGATGTCGGGTGTGTATCAGCCTGATGGCGGGCAGATTTTGGTGGATGGAAAGCCACG
ACTTTGCCTGATACGAAAACCTGCTGAGTCTTTTGGCATCGCTACGATTACACAGGAATTG
AATCTGGTGGCCACGATGACGGTGGCGGAAACGTGATGCTGGGCGGCACTCCTCGGAAG
TGGGGTTTGGTCAATTTCAAACATTTGCGCAGGCAGGCACAGGCGGCGCTGGATCTCATC

GGCGTGGATGTGGATCTGAATGCTCAGGTGGGTTCTTTAGGAATCGCTAGGCAGCAGATG
GTGGAGATCGCCAAGGCGTTGTCCATGAATGCGCGGATATTGATTTTGGATGAGCCCACT
GCAGCGTTGACTGGTCGTGAAATTGATCAGTTATTCAAAGTGGTGGATCAGCTGAAAGAA
AAAGGCGTGGCCATGGTGTATTTTCGCACTTGGATGAGATCGCGCGCATCGGCGAT
ACCGTCTCTGTGCTGCGTGATGGCCAGTTCATCGCGGAGCTGCCAGCGGATACTGATGAA
GATGAGCTGGTGGCGCTGATGGTGGGTCGTAGCATTGAAAACAGTATCCGCGTAGTGCG
CCAGAGATCGGGCAGCCACTGTTGGAGGTGAAAAACCTCAACGCGGAGGGCCGGTTACAG
GATATTTCTTGAAGTGTTCGCGCTGGTGAAGTCGTAGGCCTTGCCGGTCTTGTGGGTGCT
GGTCGCACGGAAGTGGTTCGCTCGATTGCTGGCGTGGACAAAGTTGATTCGGGTGAGGTG
ATCGTTGCTGGCAAGAAATTGCGCGGCGGATATTTCCGAGGCTATTAACAAACGGCATC
GGGCACATTCGGAAGATCGAAAAGCCAGGGCCTGGTGTGGGGTCTGTGGAGGAC
AACCTGGGATTGGCGACTTTGGCGTCGACAGCCGCGCAGGTTTGGTCGATCGATCAGGA
CAGCACAACGAGCCGCGGAGGTGCGGAAAACTCCGCATCCGGATGGCAAGCCTCAA
CAACCGATTAGCGATTTATCGGGCGGCAATCAGCAAAGGCCGTGTTCCGCCGCTGGGTG
CTTGCCGGGTCAAACGTGCTGCTTCTCGACGAACCGACCGTGGCGTTGACGTCGGCGCG
AAGGTGGAATTTACAACATCATTAATGAGATGACGGAAAAAGGTGGCGCTGTGCTCATG
GTGTCATCGGAGCTTCCCGAAGTCTTGGGCATGGCTGATCGCATTTTGGTCATGTCTGGT
GGACGCATCGCAGGCGAAGTGCAGCGAAGGGAACAACCCAGGACGATGTATGGCTCTA
GCTGTTTCCAGGTGGATGATTCCATCACCAGGAAGCTGCTGCAGAAATCGAAAACACA
AAGGAGGACCGT

>RXA00204-downstream
TGAGCACCGCCGTAGTTTCACAG

>RXA00270-upstream
TGGAGACTGCAACTGAGTTCACCTACGTGATCAACGAAGATGCAGCAGAGCGCCAGGGCG
TGGAGATCCCTCAAGAGATTTTGGATAAGGCCGAACGCGT

>RXA00270
ATGATCGGCGCTTTTGAAGTTCGGATTGTTGTACGGAGTTGTGCGATTGGGCGTCTATTTG
ACGTTCCGTGTGCTCAACTTTCCCGACCTCACCGTTGACGGCAGCCTGACCACTGGCGCG
GCAACAGCTGCGACAGCTCTTATGTCTGGCTGGCCTCCCCTTATGGCTACTGCCGCTGGT
TTCGTTACTGGCTTTATCGCTGGCATGATCACCGGTTTGCTGCACACCAAGGGCAAGATC
GATGGTTTGTCTCGCAGGTATTTTGACCATGATTGCGTTGTGGTCGGTTAACTTGCGCAT
ATGGGTGGCGCGAACGTGCCATTGTTGCGCACCGATAACCTCTTACCCCGCTTCGCGAC
GCCGGCTCCTCGGCACATGGGCAGGCCCGGCGATCCTCGCCGTTGCAGTGGGAATTTTG
GGACTCATCGTCATCTGGTTCCTCAACACTGATATCGGACTGTGCTGCGATCCACCGGC
GACAACGGGCCGATGGTGCAGTCCTTTGGTGTTCACCGATTTTACCAAATCCTCACC
ATCTCCCTGTCCAATGGTTTTGTTGGTCTTGCCGGTGCATCATCGCTCAGTACCAGGGC
TTCGCAGATATTTGATGGGTATTGGCCTCATCGTGATCGGTCTCGCATCGGTTATTTTG
GGCCAGGCCATCTCCGTGAGCGTCGCGTGTGGTTGGCTGTGTTGGCTGTATCGTCGGT
GCCATCGCATCCCGCTGATCATTTTCGACGACTGCGCGTTGGCCTTGACCCCAACGAT
ATGAAGGCAATTTCTGCGATCTTGGTGGTTGTGCGCATGCTGCTGCCAGGTGGCGTGCG
AAGTTCTCCAAGGCACCGAAGCCTAAGCAACCAGTAGCAGTGGAGGCT

>RXA00270-downstream
TAAGACATGTTATCCATCAACGG

>RXA00311-upstream
CGGACAGATCGGCATTTGGGCGACCGTGCTGTTGATGATCGCCCGCATCGCATAGGGATT
CTCTGCAGTCGCAGAAGCTGCAGGTGCATCCACACTGACC

>RXA00311
ATGGAACATTCTCCTGAAGGCAAGCGTGGATTCTTCACCTCATCGGTGATGGCGGGTTGC
TCAGTTGGAACGTCCTGGCTGGCTTGGTATTTATCCCGTTCTTGATGCTGCCGGAAGAA
CACCTCATGTATGGGGCTGGCGCGTACCTTTCTGCTTTCCGCACTGGTTTTAGTTGTC
GCATACTTCGTGCGCACCCGACTGGAGGAAGCATCAACTGAGAAGGCCGAAGAGGACGCA
GGCGCTCCGGCTTTGGCTGTGCTGCGCACCCAGGGCATTGATGTGCGACGAGTTTTCTGT
ATCACCTTCTTCGCCGTTGTTTCAGACCACTTTCAACGTTTACGCACTGGCATACGCCGCC
AACGAAATCGGCATCGATCGTTCTTCATGGTGATGGTGAACACCATCGCGCTGGGGCTT
TCCATCGGAACGATTCCTTTGGCCGCGTGGGTCTCTGACCGCATTTGGCCGAAGCCAGTC

TTGCTGTTTCGGGGCCATCACCTGTGCAATCACCACTACTTCTACTTCCAGGCAATCTCT
GAAGCTGACCTTGTGCTGATCTTCGCACTGTGCTTGGTCAACCAAGGTTTGTCTACTCC
TGCTGGAACGGCGTGTGGACCATTTTCTTCCCAGAAATGTTGCGATCTTCCGTGCGCTAC
ACCGGCATGGCTATGGGCAACCAGCTCGGTCTGATCATCGTTGGTTTCGCACCAACCATC
GCCACCGCCCTGTACGCATGGAACGGTTGGGAAGCTGTTGCGGGATTTCATCATCGGCGCA
ATCGCACTGTCTGCCGCAGTTATTTTGACCACCAAGGAAACCGCCTTCACCAAGCTTGAA
GATCTAGGGAAGAAA

>RXA00311-downstream
TAATGTCTGACAAGATCTGGAAA

>RXA00312-upstream
CCATTGAATGGGAAGAACTTGGTTGTGTGTTTGTGACACCTATTCTAAAGAACATTAAAC
GTGATTAAGTTCATGATTCTTAATGAGAAAGGGTGATCAC

>RXA00312
ATGGAAACCGTGAGGACCGCAACCGCCGCTCCTGAAACTGCATCTTTGAAGCTGCGTGAG
GCAGAAAGCCCAGCAAAGTCCCCAAAGAAAGCCGCTTGGCGTCACTTTTGGGTTGCGACT
CTGGAGTACTACGACTTTGTCAATTTACGGCACCGCCTCCGCGCTGCTGTTCAATCACCTC
TTCTTCCCACAGGGCGACCCAGTCGTGCGACGATCGGCTCTCTCGCCTCATTCGGTGTT
GCGTACATTGCGCGCCCCATCGGTGGTCTGGTGATGGGACATGTTGGCGATAAGATCAGT
CGCAAACCGCCCTCATGGTGACGTTGATGATCATGGGTATCGCCTCCATTTCCATCGGA
CTTCTGCCCACCTACGGACAGATCGGCATTTGGGCGACCGTGCTGTTGATGATCGCCCGC
ATCGCA

>RXA00312-downstream
TAGGGATTCTCTGCAGTCGCAGA

>RXA00345-upstream
AGTGACCCATATGGCGTATCCGAGGTCTAACGCGATTTTGGCATTTTCAATAAGTTTTCA
TGTTGACATCCTTTTTCAATAAGCATTTA

>RXA00345
ATGGCAGGTATGAAAAAGCTTCTTTGGACACTCCCCATCCTCCCACTGGTACTAGCTGGC
TGCTCAACTGGATCAGCAGATTCCGCGGATTCACCAACGCTGCCGGATCCAATTCCCTT
AAAGTGGTCACCTCCACCCAGGTGTGGGCTGACGTCGCCGAAGCTGTCGCCCCAGATGTA
GACATTGAAGCAATTATTACCGGTGGCGACATCGACCCTCATTCTTCGAGCCTTCCGCT
ACCGATATGGCTAAAGTTTCCGAAGCTGACATCATTATCGTCCGTGGCGGCGGCTATGAT
TCCTGGCTCTACGGCACCTTGGAAGACGATGATCGCATCATCCACGCATTGGATCTCTCA
GAGCATGACCACAGCGAGCATGATGATCAGGACGACGAAGCCGAAGAAGCCCACGAACAC
GACCAGCATGAAGAGGGCCACGATCATGACGTCGACAACGAGCAGCTCTGGTACTCCACT
GAATACGTCCTGAGGTAGCTGAAGAGTTTCGCAGAAAAAGTCACCGAGCTTGATCCCGAG
GCACAGGCCGATGCAACGGCTGTGACCACCAAGATGGACGAGCTGCACAATCAGATTAC
GATCTTCCAGCAGTTCGCATTGCTCAGACCGAGCCGATCGCCGATCACATTTTGTCCAC
TCCGACATGGTGGAATCCACCCCTGAGGGTTACCGCGCAACCACGTTGAGCGAGAGCGAG
CCAACCGCAGCAGATGTTGCGTCGTTCCAGGATGCAATTAACAACGGTGACCTCGATGTT
TTGATCTACAACCCACAGTCCGCGTCGACTGTGCGGACCAGCTTGAAGGATTTGGCAGAA
GAAAAAGGCATCCCAGTTGTTGAGATCTATGAGACCCCTCAAAACACCGAGAATTTCTC
GATGCATTACCAAGGCAGTTGATGATCTCACCGCTGCCACTAACCGGTT

>RXA00345-downstream
TAGAATTATTTAAATGCTGTTGA

>RXA00378
AAATCCTGGCGGTCATATCCGTCCTGGTTCGCTTTTGACCACGGCACGTTGACCCAAAAC
GAGATTTATTTTGATGTGGCTGCGGAATCACCGTGTGCTTCTTGCCGGACGGCTGCTG
ACAAGGCGTCGAAGCCAATCCAGTTTGTAGCGGAATTTGGTGCCTCCAAATCGATCCA
CAGCGCATTGTCACTGTGGTGCGTAAACACCGATTGAAGCGCGTAGTCCAGGAACGAAC
ATTCCAGTGACGGAAGTCCGTGTCAATGACGATGTGAAAGTTCCACCTAATACCACGATC
CCTGTGGATGGCACGTGCATCGGTGGCGGTTTCGCGGATCGCAGCTAGCATCATCATGGGA
CAAGACCAGCGTGATGTAAAAGTAAATGACAAAGTTTTCGCCGGCAGCCTCAACCTCGAA

TCCGAAATCAAGGTTTCGTGTTATTTCGCACTGGTCAACCGCACCCGCATCGCCGCGGTACAT
 AGGTGGGTTAAAGAAGCGACGTTGAAGGAAAACCGCCACAATAGGGCAGCGATCCGTTCCG
 GCCGGTAACCTTGTGCCCATCACGTTACCCCTTGCTGTGGTGGACTTCTGTCTGTGGGCA
 CTGATCTCTGGAAACATCAACGCTGCATTTACCACTACCTTGGCTGTCTTGCCTGCGTG
 GCTCCGGTGGCCTTAGCGTTGTCTGCTCCACTTGCCACGAGGAATTCCATCGAAGCTGCA
 GCACGACACGGTATTTTGGTCCGCTCTGGTGAAATTTTCCGAGTTCTCGATGATGTGGAT
 ACTGCCGTATTTAATCGTGTGGGCACACTAACCGATGGCGAAATGACAGTGGAACCGTC
 ACAGCAGACAAAGGCGAGGACCCAGAACTAGTGCTGCGTGTGCGCGGGGCGTTGGCCATG
 GAATCCCACCACGCGATTTCCAAAGCACTGGTGAAAGCATCCCGTGAAGCTCGTGATACC
 GGCGCCGGTGGTGAAGATGTCCACACTGGATTGAAGTAGGCAACGTGGAATCACCAGAA
 GCCGGCTCATTCCAAGCAACCATCGAGCTGCCACTGATCAAACCATCTGGCGAAAAAATC
 ATGCGCACACAGAAGCACTCCTGTGGCGACCACGATCCATGACAGAAGTCCGTGAGCAC
 TTAAGCCCCCGACTAGTGGCAGCAGCAACCTCAGGTGGCGCACCACTGATCGTGCGATGG
 AAAGGCAAAGACCGCGGAGTTATCACTCTAAGTGACCACGTGAGATCAGATTCCCTCCGAT
 GCGATTATTGCGATTGAAGAACAAGGCATCGAGACCATGATGCTTTCACGTGATACTTAC
 CCGGTGGCACGTGATACGCAGACAGCTTAGGCATCACCCACGTCTTGGCCGGCATCGCG
 CCGGGCAAGAAAGCCAGGTCTGTCGTGCAGTCCACACCCCGCGGATCCACTGTGCGGATG
 ATCGGCGATGAATCAGTAATGGACTGTTTGAAAGTCGCTGACGTGGGTGTACTGATGGGC
 GTCGATCGTCCCTCAGATCTGCGTGATGATTCCGATGACCCGGCAGCTGACGTTGTGGTC
 ATGCGCGAAGAGGTGATGAGCGTGCCGACGCTGTTTAAACTGGCTCGACGCTACGCCAAG
 TTGGTCAATGGCAATATTGCTCTGGCCTGGATCTATAACGGTGTGTCATGGTGCTTGCA
 GTGTCTGGCTTGCTGCATCCAATGGCTGCGACCGTGGCTATGCTGGCGTCTTCGCTGCTT
 ATTGAATGGCGCTCGGGCAGGGCGCGCAAGTAC

>RXA00378-downstream
 TAACCAGCAATTCCCAAGCCCAA

>RXA00412-upstream
 CTTTTGACGAACACCACGTGCGGTACGCTTCCTCGGGGCGTTAAACTATTTGTCTTCCAG
 CTTTTGTCCCCGACTTTTGTACGAATCGAGGACACCGTC

>RXA00412
 GTGTCACACACCGCGTCCACACCGACGCCAGAGGAATACTCCGCGCAGCAACCCAGCACC
 CAGGGCACTCGCGTTGAGTTCCGCGGCATAACCAAAGTCTTTAGCAACAATAAATCTGCT
 AAAACCACCGCGCTTGATAATGTCACTCTCACCGTAGAACCCGGTGAGGTAATCGGCATC
 ATCGGTTACTCTGGCGCCGGCAAGTCCACTCTTGTCCGCCTCATCAATGGCCTTGACTCC
 CCCACGAGCGGTTGCTTGTCTCAACGGCACCGACATCGTCCGAATGCCCGAGTCTAAG
 CTGCGTAAACTGCGCAGTAATATCGGCATGATTTTCCAGCAGTTCAACCTGTTCCAGTCG
 CGTACTGCGGCTGGAATGTGGAGTACCCGCTGGAAGTTGCCAAGATGGACAAGGCAGCT
 CGTAAAGCTCGCGTGCAAGAAATGCTCGAGTTGCTCGGCCTGGGCGACAAAGGCAAAAAC
 TACCCCGAGCAGCTGTGCGGCGGCCAGAAGCAGCGCGTCGGCATTGCCCGTGCACTGGCC
 ACCAATCCAACGCTTTTGTCTGCGACGAAGCCACCTCCGCTTTGGACCCAGAAACCACC
 CATGAAGTTCTGGAGCTGCTGCGCAAGGTAAACCGCGAAGTGGGCATCACCATCGTTGTG
 ATACCCACGAAATGGAAGTTGTGCGTTCCATCGCAGACAAGGTTGCTGTGATGGAATCC
 GGCAAAGTTGTGGAATACGGCAGCGTCTACGAGGTGTTCTCCAATCCACAAACACAGGTT
 GCTCAAAAGTTGCTGGCCACCGCGCTGCGTAACACCCAGACCAAGTGGAATCGGAAGAT
 CTGCTTAGCCATGAGGGACGCTCTGTTACCATTGATCTGACTGAAACGTCCGGCTTCTTT
 GCAGCAACCGCTCGTGCTGCCGAACAAGGTGCTTTTGTCAACATCGTTACGGTGCGGTG
 ACCACCTTGCAACGCCAATCATTTGGCAAAATGACTGTTGACTCACCGGCAACACCGCT
 CGGATTGAAGAGTTCTATCAAACCTTGACCAAGACCACGACCATCAAGGAGATCACCCGA

>RXA00412-downstream
 TGAACGAGATGATCCTCGCAGCT

>RXA00413-upstream
 CTGTACAGATCGCGGTCTATGGTGCTAATCTCCTAAATACTTGAATGACCATTTCATGAT
 CCATTACAAAACTTTCCCAAACAAGGACGTATTTGAAA

>RXA00413
 ATGAAACTTCGTGCGATCACAACCACCGCCATCGCTGGCCTCTTCGCCGCAACCGCACTT
 GTTGCCTGTGGCTCCGATTCGGATGGAAGCAGCACCACTGTTGCTGAAGGCACCGAAGGC

GTGACCATCCGCATCGGGACCAACCGACGCTGCGAAGGAAGCATGGACCGTATTCTGAAGAC
AAGGCAGCTGAAGAGGGCATCACCTCGACATCGTTTCCTTTCTCTGACTACTCCACCCCA
AATGAGGCTCTTGCCAGGATCAGCTGGACGTTAACCTCTTCCAGCACCTGAAGTTCTCTG
GCTGAGTACAACGTCGGCTCCGGCGCAGACCTCACCCAGTTGGCTCCAGCGAAATCGTG
CCACTGGCACTATTCTGGAAGGACCAGACTCCATCGACGGCATTGACGGCGAGTCCGTT
GCCATCCCTAACGATCCTTCCAACCAGGGCCGCGCCATCAACGTTCTCGTTTCAGGCAGGT
CTGGTCACCCCTGAAGACCCAGGTCTGGTCACCCAGCTCCAGTCGATATCGACGAGGCA
GCTTCCAAGGTTTCCGTCATCCCAGTCGACGCAGCTCAGGCACCAACCGCTTACCAGGAG
GGTCGCCCAGCGATCATCAACAACCTCCTTTCCTTGACCGCGCAGGCATCGATCCAAACCTC
GCGGTCTTGAAGATGATCCTGAGTCTGAAGAAGCAGAGCCATACATCAACGTCCTTCGTC
ACCAAGGCTGAGGACAAGGACGATGCCAACATCGCCCGCCTCGTTGAGCTGTGGCAGCAG
CCAGAGGTTCTGGCTGCAGTAGACCGCGACTCTGAGGGCACCTCCGTCCAGTTGATCGT
CCAGGAGCTGACCTTCAGGAAATCCTTGATCGCCTTGAGGCTGATCAGGAAAACGCA

>RXA00413-downstream
TAATCTCTTTTGAGTTCTTTGCA

>RXA00431-upstream
TGGATCGTCCTCGCCTTCACATTCGTGCGCCTTGCCCTTGCTCTCCTCGCGATGAAGCAA
TGGCGATTCCGCGTCAGCTACTGGGTATAAGGAGCACCAC

>RXA00431
ATGGTATCCATCGATACATAACAACGCCTGCGTCGACTTCCCCATCTTCGACGCCAAATCC
CGCTCCATGAAGAAAGCCTTCTCGGGCGCAGCCGGCGGAGCAATCGGGCGCAATCAAGAC
AACGTCGTAGTCGTGCAAGCGCTGAAGAACGTCAACCTGCACCTGCGCGAAGGTGACCGG
GTCGGACTCGTCGGCCACAACGGCGCCGCAAAATCCACCCTCCTGCGACTCCTCTCCGGC
ATCTACGAACCCACCCGCGGAAGCGCTGACATCCGTGGACGCGTCGCCCCCGTCTTCGAC
CTCGGCGTCGGCATGGATCCAGAAATCTCCGGCTACGAAAATATCATCATCCGCGGCCTC
TTCCTCGGTCAAACCCGCAACAGATGAAAGCCAAATGGAAGAAATCGCCGACTTCACC
GAACCTCGGCGAATACCTCTCCATGCCTCTCCGAACCTACTCCACCGGCATGCGCATCCGC
CTAGCCCTCGGCGTGGTCACCTCCATCGAGCCCGAAATTTCTGCTTCTTGATGAAGGCATC
GGCGCCGTCGACGCCGCCTTCATGGCCAAAGCCGCGACCGGCTCCAAGCCCTCGTCGAA
CGATCCGGCATCCTCGTCTTCGCCTCCACTCAACGACTTTCTTGCCAACTCTGCAACACC
GCACTCTGGGTCGAC

>RXA00444-upstream
GATCGTGCCAAGGAGATCCTTGCCAGCnnnnnnnnTnnnAntGGTTTTGGCACAAACTAA
AAAGGCTCGTCGAAGCGAGAATCATATCCTCCCAGGGTGG

>RXA00444
TTGCTCATCCCAGCCACCCTGGCCATGCTGCTGATCATTGGACCTATTTTTGCTTTGCTG
TTGCAGATCCCCTGGGATCGGTCTTGGGAGTTGCTTACCGCGCCGGAATCTTTAGGAACC
GCACGGTTATCTATCGGAACCTGCTCTGTTTTCTACCGCGCTATGCGCAATTGTGGGTTTC
CCGCTAGCGTTGGCGCTGCATTTATATGAGCGTTTCGCACCCAGGGTGACATCAGTTTTG
ACGGTGCTGGTTTTATGCGCCTTTGGTGTGTCGCCGGTGGTGTCTGGTTTGGCGCTGACT
TTTCTGTGGGGCAGGCGTGGTTTTTTAGGTTCTTGGCTTGATCAGGTTGGATTGCCGATT
GCATTTACCACCACGGCTGTGGTGTGTTGCCAGGTGTTGTAGCGTTGCCATTTTTTCATT
TCCACTGTGACTACTGCACTGCGTGGCATTCCAAAACAGTTTGAGGAAATCGCAGCTACT
GAAGGCGCAACCCGCTGGGAGATCATGCACAAGATGATCATTCCGCTGGCGATGCCTGGA
ATTTTCACCGGTATGATTTTGGGATTGCGCAGGGCCTTGGGCGAGTATGGTGCGCACTG
ACTTTTGCTGGAATATTGCAGGTGTTACCCGCACCATTCGGTTGCATATTGAGCTTGGT
TTGAGTTCCAATGACATGGATAAAGCCTTGGGAGCGGTGATTATGCTTTTGGCTGTCTAT
GTCCTCATCATTGGAGCCATCGGAGCGTTACGATTGTTTTCCAAGGTGAGAAAGGTT

>RXA00444-downstream
TAATTGATGTCTCGTTCGCCGA

>RXA00445-upstream
GGTGCAAAAAAGGACTAACC

>RXA00445

ATGGCGGATCTGAGCATTGAACACGTATCAAGGTTTTTCGGCGATGCCATCGCCTTGAAC
 GATGTGTCATTGACCGTCCCCTCAGGCTCCATCACCGCCATCATCGGGCCGTCCGGGAGC
 GGTAACCACGTTACTGCGTTTTGCTGGCAGGCCTTGATTACCCGATGAAGGCACCGTG
 AGCATTGGGAATAAGATCGCCAAGCTGGGTGACACTGCGCTGTGTTTCCAGGATTGCGCT
 TTGTATCCGCACCTTAATGTGTGGGAAAACGTGGCATTTCGCTCAAGCTCAAAGCCACC
 AATACGTCAGATGAGGTGGTGAAAAAGCGGGTGAGTGATGTTTTGGAAATGCTCGAAATT
 GCTCCCTCGCCCGCCGAAAATTACCGAACTCTCCGGCGGGCAAAAACAGCGCGTCGGC
 ATTGCTCGAGCACTGGTCAGAGACGTAGAGGTTTACCTTTTCGACGAACCGATGGCCAC
 CTCGACCAAGCCTTAGCCCGCGATATTGTGGCCGATCTGCGCAAAATTCAACAATCGTTG
 GGACTGACGTTTTGTATACGTCACCCACAGCAAAATCCGAGGCATTGCGCTCGCCGACCAA
 ATTGTGCTGCTGGTAGATGGCCAAAGTCGCGCAGGTTGGTGAGGCGGAGGAGCTCGTCGAA
 AAGCCAAAACCTTAGAAATAGCCGAGTTCCTCTCCCCACCGAGCTCAATGTGCGCCGG
 CGTGGGACGCCGTGGAGGCATGGCGACCCGAAGACACCCAGCTCGCCCGCGGTGGCACT
 GCGACCGTGGAAGCCGTGACGTATTTGGGCCGCGAGTGGCTGTACAAACCACCGAGGGG
 CACGCCGTGTCGGAGGAAAATTGACGTCGGCGAAAGCGTCACGCTAACCCAGAAGAAG
 GTGTTTAGTTTC

>RXA00445-downstream
 TAGCCGCTGCAAAAGGAGGGAG

>RXA00466-upstream
 TTTAAAGCGCACTAAGAGCTCGTCAATTCTTTAAACAAGCTGAGAATGTGAATAATAG
 GATAGTTAACCTGATTCGATTAGAAAACGGAGATTTGTC

>RXA00466
 GTGCAATCCCGCCTGTCCAAAATCCTGCGCAGTAGCGTCGTAGGCGTTGCTGTCTTAGCC
 CTGTTAGCTGGGTGTTCTAACAATGCAGATGACACCGACGCTGATTCAACATCCACGGGA
 AACTCCGCTTTTCCTGTTTCGATTGAACACGAGTTCGGAACCAACACAATCGATGATGA
 CCCGAAAGAGTTGTCACCTTGGCGTTACCGACGCCGATATTGTCTCGCATTTGGGGACC
 GTCCAGTAGGCAACACCGGATACAAATTCCTCGAAAACGGATTGGGACCGTGGACTGAT
 GAGTTAGTGGAAGGCAAAGAATTAACACTGCTTGACTCTGATTCCACACCAGATCTTGAA
 CAAGTAGCAGCCCTGGAGCCAGACCTGATTATTGGAGTCTCTGCGGGGTTTGACGACGTT
 GTATACGAGCAACTATCTGATATCGCACCGGTGGTCGCCCCGTCCAGCGGGAACAGCTGCA
 TACGCACTAGCTCGCGAGGAAGCTACCAACCTTGTGCCCCGTGCGATGGGGCAATCAGAA
 AAAGGACAAGAGCTCAATGAGGAAACAGATGCTCTGATCCAAGCTGCGCGTGATGAAAAT
 CCTTCTTTTGACGGTAAACAGGAACCGTCATCTTGCCATACCAGGGTAAATACGGTGCC
 TACCTGCCAGGCGATGCACGGGGACAATTCCTCGATTCACTTGGCATTTCGCTGCCGGAA
 GCAGTTCTTTGCGGAGACACCGGCGACAGCTTCTTTGTCGATGTCCCCGCTGAAAGCGTC
 AAAGACGTAGACGGTGATGTTCTCTCGTGCTTTCCAACGACGAAAATCTGGATATCACA
 GCAGAGAATCCACTGTTTGAAACACTCAACGTTGTGCAAAAAGACGCAGTAATTGTGGCA
 ACAACCGAAGAACGCGGGGCGATTACCTACAACCTCAGTGCTGTCTGTTTCTTTGCGTTG
 GAACATCTCGCACCACGTATTGCTGAG

>RXA00482-upstream
 GCGATTTCTATGAAATTCTTCACCCATCCACAACCTATCTACTATACTTTTAGAAGTAATA
 ACTATTGAGTTAATATAAACATGAAGAAAGGATTTGCTTT

>RXA00482
 ATGCGCATTTCAAGCAAACCTTGTCACCACAGCACTACTCGCAGCCATTTCACTTTTCGGG
 ATATCCACGGCACAAGCCCAAGACATTTTTGACGGCGGACGACTTGACAGGTGGCTCCTCG
 CAGGTATCTAACCTAAGTTCGGTTTCTGAAAACCTAGCGCTGCCCGAAATTGAAAATAGC
 ATTTACCTAGAACGCTACAAAGGCAAGTGGTATCAAGTCGCAGCAATTCCCCAACCATTC
 TCTTTACAGTGCTCACATGACGTTACCGCTGATTACGGCGTGATCGACTCGGACACAATC
 TCTGTAACAAATAAGTGTGGCACTTTCTTTGGGCCTTCAGTTATTGAAGGCAGCGCTAAA
 GTAGTTTCCAATGCTTCATTAAAGGTTAGCTTCCCAGGTATTCCATTTTCAAGTGAAGAC
 AATCAAGCAAACCTACCGCGTGACCTATATCGAAGATGATTATTCACTAGCAATCGTCGGC
 AGCCCAAGCCGGTCTCAGGATTTTACTATCCCGCACGCCACAGCTCAGTAGTGACCAA
 TGGTCTCACGTTCCGAACATTACAGAGGACAGTGGGTGGTGGCCATGCGCATTCATTACA
 GTCCAGCGACAGGTGGCTTAAACACCGCCACTCCGCTCTGCACACTT

>RXA00482-downstream

TAATTAACGTAGATGGTCATCTA

>RXA00523-upstream
TGGCGCGGCGGGCGTGAATTTTTCAGACG

>RXA00523
GTGTTGCGTAATCAGTTGGCGTCGCCGATATTATCGGCATTTCTTCTGGCGCGTCGGCG
GCGGGCGTAATTTGCATTGTGTTTTTTCGGAATGTGCGAGTCTGCAGTGTGCGGCGATTTCT
TTGTGTGCGTCCTTGGCTGTGGCGTTGTTGATTTATCTGGTGGCGTATCGCGGTGGTTTT
TCGGCCACGCGTCTGATTCTTACCGGCATTGGTATTGCTGCGATGCTGAATTCATTAGTG
TCGTATTGCTGTCCAAGGCTGATTCTTGGGATCTGCCGACCGCGACGCGCTGGCTTACC
GGCTCGCTCAATGGTGCGACGTGGGATCGTGCGATGCCGCTGATTGTCACCACTGTGGTA
CTCATTCGCTGCTGGTGGCTAATGCGCGCAATGTGGATCTTATGCGTTTGGGCAATGAT
TCCGCGGTGGGTTTGGGCGTTGCTACTAATCGCACGCGCGTCATTGCGATTATTGCCGCT
GTTGCGCTCATCGCGTTGCTACCGCTGCATGCGGCCCCGATCGCATTCGTGGCGTTTGTG
TCTGGCCCCATTGCCGCGCGCATTTTAGGCTCCGGCGGATCGCTCATCATCCCCCTCCGCA
CTCATCGGCGGGTTGATCGTGCTCATCGCCGACCTAATTGGCCAATACTTCCTCGGCACC
CGCTACCCCGTCGGAGTTGTCACCGCGCATTCGGCGCCCCATTCTTATCTATTACTC
ATTCGTTCCAACCGCGCGGGAGTAACCTG

>RXA00523-downstream
TGACCACCAACCATCAACTATCC

>RXA00525-upstream
CCATCGTGTTTATTACTCACAACCCTGAGCTTGCTGATGAATCTGATCGGGTGGTCACCA
TGGTTGACGGGCGCATCATTGGGTCTGAGGTGAAACACTC

>RXA00525
ATGAGCCTTGCGAATCAATTCTTTTGGCGCTCACCAGCCTGAGAAGCAACAAGATGCGT
GCATTGTTGACGCTGTTAGGAGTCATCATTGGTATCGCATCAGTCATCGGAATTTTGACC
ATTGGTAAAGCCCTGCAGGATCAAACCTTTGAATAGTTTGGAAAGCTTGGGCGCGAATGAT
CTGTGCGCGCAGGTGGAGAACGCCCGACGAAGATTCCCCCGAACCCGATATGTTCCGCT
TTTTCTGGGGCTGCAAACCTCTAGTGGCAATCTGATTCCGGAAGAAACAGTTGATACGCTG
CGCGATCGTTTCGCGAGGAGCATCACGGGAATCAGCGTTGGCGGAATGGGTACGCAAGGC
ACTCTCATCGGCGACACCGCAGATCTTAAATCCGATCTCCTCGGCGTCAACGAGGATTAT
ATGTGGATGAATGGCGTCGAAATGAACACGGCCGCGCCATCACGCAAGACGATGTTGCC
GCTCAGCGCCCCGTTGCGGTCATCGCCCCAGACACCTTTAATACGCTTTTCGACGCAAAC
CCCAACCTCGCTCTGGGGTCCGAAGTAGCTTTTGAACCAACGGTCAAGAGACATTTTGT
CGGGTTATCGGTGTGTATAAAGAAGCCGACGAGGTGGACTTGTGGGAAGCAATCCAACC

>RXA00556
TACACCCCATATACGGTGGCCAATGACATCACCCACACGAAAGATGGATTGAACACGTTA
AGTATCCGTGCAGCTCAGGGCGTAGACCAGGATTCACTTAAGGGTTCACTGCAAACCTAC
TTCGACGCGCTGTACGCCAACAATGACTCGCACACGTTGCCATGTTGGACTTCCGTAAA
CAGATCGAAGAGTTCAACACCATTCTCGGCGCAATGAGTTTGGGTATCTCAGCCATCGGC
GGAATTTTCTTGGCTTGTGCGGTGGCATCGGAGTGATGAACATTATGTTGGTGTCTGTCACC
GAGCGAACCCGCGAAATCGGTGTCCGAAAAGCCCTCGGCGCTCGTCGACGTGACATTCGC
CTGCAATTCGTGCTGAAGCCATGATCATTGTTTCATCGGTGGCATCCTCGGCGTGCTT
TTGGGCGGCATTTTGGGATTGATCATGTCCAGCGCTATTGGCTACATTTCTTGGCACCA
CTGAGTGGAAATCGTGATCGCCTTGGTAATTTCCATGGCTATCGGCCTGTTTTTTCGGCTAC
TACCCCGCCAACAAGGCAGCAAAGCTCGATCCAATTGACGCCTTGCGTTATGAG

>RXA00556-downstream
TAAAAGCCTCGTTTTTAAGGTAG

>RXA00596-upstream
CCGCCACCGACGGCCTCTTGAACACCGATGCATACCAACAGGCTGTGCTCGGTGAAAATG
CCATCGGAGTGCCAAGCCCTAGCTACCAGGGAGGAACTA

>RXA00596
ATGCTTAACGCCCTGAAATTCATCCCATGGCTGATCGGCCAGATTTTCTCTCTGGCTTC

AGCGTGATCACCGCTGCGGTAAAAAAGGACACCGGCTTCAACCCCGTTGTTATCCGCTAC
 CCACCTTCGAGTGACCACGGACTTCCAGATCGCAGCCCTGTCAACGTGCATCACCGCGACT
 CCTTCCACCCTGTCCCTTGGCCTACGCGAACCCCGCAAGCCCGGCGACCCACCATTG
 CTGATCCAAGCAGTGTGTTGGTTCCGATCCAGTAGAAGTTTTGAATCCATCGCCGATATG
 GAACAACGCCTCGTCCCTTCGGTCGCTTCAATTGACCACGGCGTCCCAGGCCAAGGCCCT
 TACAAGGAGATCCGCCCCAGCGATGCTGAGTGGCCAAGTCGCGAGATCGCTGACACCGCC
 CAAAACACCGCTCAGCCAAGACAAGAGGGAGTTT

>RXA00596-downstream
 TAAAACAACATGACTGCTTTTGG

>RXA00634-upstream
 AAGTGTGTTTTAATTACCGCAGCTTTGTCTTAGGAGAAGTCATGGTCCAACTGGATCAACG
 GGTTAGGTTCAAAGCGCAACCTCAATAATCAGTATTGAA

>RXA00634
 ATGTGGGAGCGATTAGCTTCTACGGCATGCAAGCACTCTTGGTGTACTACCTGTATTTT
 GATGTTGCAGCCGGTGGATTAGGCCTTGATCAAACCCAAGCAACAGGACTGGTCGGCGTT
 TATGGCGCACTGCTCTACCTCTGCTGTTGGGCAGGCGGTTGGGTCAAGTACAGAGTCCCTG
 GGCGCAGAAAAAACCTGCTGGGCGGTGCGATCTCAGTAACCATCGGACACCTTGTGCTT
 GCTGGCCTCGGCGGGAATTTGGTCTAGCCATTGGCCTTGGATGCATCGCGATCGGTTCA
 GGATTTGTGAAAACAGCAGCCATCACCGTCTGTTGGGATCCAGGCATGGTGAACAAGAAGGA
 GACGCAAAGGCAGATCCCGCATTCCTTCTACCTAGGCATCAACGTTGGTGCAGTCTG
 CTCGGACCACTCCTGACCGGTTGGCTCTCCAGCAGGTATTCCTTTGAAATGGGATTTCGGC
 GCAGCCGCAGTCTTATGATCGGCGGATTGGGAATCTACGCAGCGTTGCGGAAACCAATG
 CTGCAATCGTTCCTGCTCGAGGTGAAGAAAGCGTCTCGCGCGCCAAAACCTGCAGAA
 AAACATGTGATTAGCACGGCATTTGCTGCAAGTGGCTGTGCTTTGCGGAGTGCTGCTTTAT
 CTTCTCCTTACAGAAACAGTCAGCGCAGACCAACTAGCTGGAGCTCTGCTTTTAGTAACA
 ATCGGTGCAGCACTATGGCTCATTATCCAGCCCTTACGACACCCACAAGTCAGCTCCGAA
 GAGAAACGAAAAGTGCTGGCATTCATCCCGATCTTCGTCTGCTCAACCGCATTCCTGGGCA
 GTGCAAGCACAAACCTACGGCGTACTAGCTGTGTACTCCCAAGAACGTGTTGACCGCATG
 GTTGGCGATTTTGAGATCCCGAGCAGCCTGGTCACAATCACTCAATCCTTTTTTTCATCCTG
 GCGCTGTCCATCCCGATTTCCCTGTGGTTTATGCGCGGATCACGCGCCCCAAGAGTGAAA
 ATTGGAATCAGCATTTGGAGTGATCATTGCGGGAAGTGGGCTTCTAGTTCTTATTCATTT
 GTTGGAAATGCCGCTCGCGCAGTGTGGGTGCTGCTTTAAGTGTGTTTCTCATCTCACTG
 GGAGAACTTTTCATCGGACCCGGAGGAATGGCTGCGACTGCGCACCACGCACCAACGAATA
 TTTGCCACACGATTCTCCGCCCTGTATTTCTCACACTCGCCATCGGCATGTCTATTGCA
 GGTAATGTGTCCAAATTTTACGACCCCAACCAACACCTCCGAGCTCCGATACTTCGCG
 GTATTTGGCATTTTCGATCATCGTCATCGGTGTGCGTTCACTGATGGTGGCCAAGAAGGTT
 GGA

>RXA00634-downstream
 TAACAGGGTTAATCTTGGGTGAT

>RXA00665-upstream
 ACCAAACACTTCTGTGCGTGACACGCGCCACCTTATACTCCCAAGCAACACAGAACAC
 TCGGGATCTCAAAGTTTCGAGAAACACAGAAAGGGCAGCA

>RXA00665
 ATGAGCAGCTCAACACTTCTCCTGGCTTCAGGACAAGTCACGGCATTAGCCGCTGACTAC
 ACGCTCAGCCACACCCCTCAGATGGCATCCTGGTAGTCCTTGGCTTCGCCATGATCCTC
 ACCCTCATGACCTGATCATGTGGGTGACTCACCCCAATGGTGGCCATGCTGTTGGTC
 CCCACCATCTTCGGTCTCATCGCGGCGCAGGACTCGGCCTTGGTGACATGGCGCTTGAC
 GCCATCAAGGACATGGCGCCTACCGCGGCACTCCTGATGTTGCGGATTATGTTCTTCGGA
 ATCATGATCGACGTCGGACTCTTCGACCCCTGATCCGCGTGATACCCGCGTTCTTCAC
 GATGACCCCGCAAAGTCTGTCATCGGCACCGCAGTACTTGCAGGTGTTGTCTCCCTCGAC
 GGCGACGGCTCCACCACC

>RXA00702
 TTAGGGCTCCACCTGCGGTCATGCGCAAGCGCGTAGAGGAAACCCTTGATCTTTTAGGC
 ATCGCGGAGCTGCGATACGTGCCATTGGCGGAACCTATCTGGTGGTGAGCAGCAGCGCGTG

GCGATTGGCGCGGTGCTGACCACCTCGCCCCGCGCTGATTATCTTGGATGAACCAACCAGC
 GCTTTGGACCCTAATGGTGCCGAGGATGTGCTGGCAACCGTAACCAAGCTGGCTCATGAC
 TTGGCGATGACCGTAGTGCTTGCTGAACACCGCATCGAGCGCGTACTGCAGTACGTGGAC
 CGCGTGGCGCATGTGGGCGCTGATGGGCACGTCACTGTTGGGACGCCGGAAGAAATCATG
 GCTGATTCTGATGTGGCACCACCCATTGTGGAATTAGGACGCTGGGCTGGCTGGGCTCCC
 CTACCGCTATCGATCCGCGATGCACGCGCACACTCCGCTGACATGCGCAAACGCCGTGTAT
 CAGCGTGGTTTGTGTTGAACAAATTACACAACCACGCTGTCCAGCCACTTTTGATCGCC
 GAAGATATCATGGTTGATTTCCCCGAAATCCGTGCCGTTGACGGCGTGAACCTGAATCTC
 AACTCCGGTGAAATTACCGTGCTCATGGGCCGAAACGGCTGCGGAAAATCATCCCTGCTG
 TGGGCTTTACAAGGTTACGGGACTAGAAATCAGGGCTCGGTGCAGGTGCTTGATGAGGCC
 GCGGGATTTTCGTGGACAGACCCCAAACCTTTAAAGCCCCGCAAGCGGCGCAATCTTGTG
 TCCATGGTTCCGCAAACACCGACCGATATTTTGTATGAATCAACCGTGCATGCAGAGCTC
 GCACGCTCTGATAAAGATGCCGACGACCCGCCGACACGCGGGAAATCCTGGATTCA
 CTGGTCCCGAATATCCCGGACCATCTCCACCCACGTGATCTATCAGAAGGCCAAAAGCTC
 TCCCTCGCGCTGTCCATCCAACCTCGCCGAAAACCCCGCGTGGTATTTTTCGACGAACCC
 ACCCGCGGCCCTAGACTACGACGGCAAGAAATCCCTCGCCCGCTCCTTCCAACAACCTCGCA
 GACGACGGCCACGCCATTTTGGTGGTCACCCACGACGTGGAATTCTCTGCACTGTGCGCC
 GACCGAGTGTTGTTTATGGCCTCTGGAAAGATCATCTCCGATGGCACAGCCGTAGAAATC
 CTCCCCGCATCACC GGCTTACGCCCCACAAGTCGCAAAAATCACC GGCGCATCCAAGAG
 GAATCACACTGGCTCACAGTCTCGGCCGTGAAAGCTGCGCTAGGGCATGGTGAATCTCA

>RXA00702-downstream
 TGATCAACGCCATCACACTCAAG

>RXA00728-upstream
 GATTACTTCACAGATGTCAGATCTTAATCAAGGGCCTGGAGCTTCAACGGCCCAACCGAA
 ACCGATTGAAGCCAAGCCACTACGCCACCCTGGCCGGTGG

>RXA00728
 GTGGCAGCCGCTATCATCGTGGCACTGCTCGCATGGTTTATCATCAGCGCGCTCAACAAT
 GAGGCCTACGGTTGGGATACCTACCGCTCGTATCTTTTGGACACCCGCATTGCCACCGCG
 GCACTTCACACCATTTGCGCTGACCTTGCTGTCCATGATCTTGGGTGTGGTTCTCGGCGCA
 ATCTTGGCCGTATGCGTATGTCCGGCAACCCTGTATGCAGGGCGTAGCGTGGCTGTAC
 CTGTGGATTTTCCGCGGCACCCCAATTTATGTGCAGTTGGTGTCTGGGGCCTGCTGGGT
 TCCTTGTACCAGTCGATCAACCTCGGTTTCGAGAGATCGATCTGCAAAGCTTGCTGTCT
 AATATGTTCTGCTCGCGGTGATCGGTCTGGGTCTCAACGAGGCTGCGTACATGGCGGAA
 ATCGTGCGCTCGGGCATCCAAGCGGTGCCTGAGGGCCAGATGGAGGCGTCGAAAGCTTTG
 GGTATGAACTGGTCAATGACCATGCGTCGCACCATCTTGCCGCAGGCCATGCGCATCATC
 ATTCCGCCAACCGGCAATGAACTGATCTCCATGCTCAAGACCACCTCTCTGGTTGTTGCG
 ATTCTTATTCTCTCGAGCTGTACGGCCGACGATGGATATTGCGTACTCCCTCTTCGAG
 CCAGTTCCAATGCTTCTGGTTGCTGCGAGCTGGTACTTGGTCATCACCTCTATTCTTATG
 GTTGGTCAGTACTACCTGGAGAAGCACTTCGAAAAGGGCAGCACCCGCACCCCTGACCGCA
 CGTCAGCTCGCT

>RXA00732-upstream
 TCTTTGGCAAGGTAGTGAACTTCTCTGAGCGTGAGATGGGTCAATTTGGCGCACCCGTCG
 CTGATCACCCCGAAACACCAACGATGTGCAGCAGGTTAG

>RXA00732
 ATGCTGGTGAGATGACCTCCACTTTGATGATTTCCGCCCGATGCTGGCCATTGGTGGC
 ATCATCATGGCGGTGCGTCAGGATCTTGGTTTGTCTTGGCTGATGGTGGTCAGTATTCCG
 GTGCTCATCATCGTGGTGGCGCTGATCATTGTGCGCATGGTTCCGTTGTTCAAACCATG
 CAAAAGCGCATTGACCGCATCAATCAGATTATACGCGAGCAGCTACCCGTTATCCGCGTG
 ATCCGCGCGTTTCGTGCGTGAAGATGTGGAACGCGAACGATTACCACTGCTAGTAAAGAT
 GTCGCTGATATCGGCGTGCGCACCGGTAACCTGATGGCGTTGATGTTCCCTGCCGTGATG
 CTGATCATGAACCTTTCTGCCGTTGCTGTGATTTGGTTTGGTGGCTTTCCAGGTGGAATCC
 GGCAGAGACGAGATCGGTACGCTCTTTGCATTCTTGCAGTACATCATGCAGATCCTCATG
 GCGCTCATGATGGCAGCGTTTCATGTTTGTGATGGTTCCGCGCGCTGCCGTTTCCGCTGAT
 CGCATCGGTGAGGTTCTGGAAACCAACCGTCTGTGACGGCGCCAGAAAACACCGGCGCAG
 CCGTCGACAAGCGCTGGCGAAATCGTGTCAACAACGCGACTTTTGCCTACCCCGGCGCG
 GATGACCCCGTGTTAAATAATGTGAGCTTCCGCGTTGCGCCTGGTAGCACGACGGCGATC

ATCGGCTCGACGGGTTCTGGGTAAGACGACGTTGATCGGGCTGGTTCCTAGGCTTTTCGAC
GTCACCGAAGGCGACGTTACCGTCGATGGCACCGATGTTCTG

>RXA00734

AGGCACCTGCGTTATGGCAATGAAGATGCCACGGAAACGCAGCTGTGGCAGGCGCTTGCA
ATTGCTCAGGCGGCGGACTTTGTGCGTGAGATGCCAGAGGGTCTTGATTCTGAGATTGCT
CAGGGTGGAACCAATGTTCTGGTGGTCAGCGCCAGCGACTAGCCATTGCCAGGGCGTTG
TTGAAGCAACCTGAGATCTATATTTTCGACGATTCTTTCTCCGCCCTCGATGTGAGACA
GACGCCGCTCTTCGCCGAGCGCTGAGACCAACCTGCCGGATGCAACCAAGTTGATTGTC
GCCCAGCGTGTGAGCAGATTGAGATGCCGATCAGATTGTGGTGCTTGATAACGGCGAG
GTTGTGCGTATTGGAACGCACACGAATTTGCTGAACACGTGCGGTACCTACCGTGAAATT
GTTGAATCCCAAGGACTGCGCAGGCGCAATCA

>RXA00734-downstream

TGAGTAATACTGCAGGCCCCCGC

>RXA00759-upstream

TCACCTGAACACTTAAACATAACTTCATCCGGCGCTTTATTAGCTTGAAGCGCCCCGC
ACCATAATCCATTCCCCAGCAAGCAAGGACACCCACGCTC

>RXA00759

ATGCTTCGTTACGTCGGGCGACGTTTGCTCCAAATGATTCCGGTCTTTTTTCGGAGCGACC
TTACTGATTTACGCCCCGTGTTCTCATGCCTGGTGACCCAGTCCAGGCATTGGGAGGT
GACCGCGGCGCTAACCGAGGCTCGGGCCGAGAAAATCCGTCAAGAATACAATCTTGATAAA
CCCTTCATCGTTCAATACCTCCTGTACATCAAGGGCATCTTCGTCTTAGATTTTGGAACA
ACCTTCTCTGGTCAGCCAGTTATTGATGTGATGGCCAGGGCCTTCCCCGTCACCATCAAA
CTCGCCATCATGGCCCTGCTGTTTGAATCAATCCTCGGCATTATCTTTGGTGTCATCGCA
GGTATTGCGCCGCGGAGGAATCTTCGACTCCACCGTGCTGGTCTTTCTCTGATAGTCATC
GCAGTCCCCACCTTCGTCAATTGGTTTCGTGCTGCAGTTCTTANTCGGCGTGAAATGGGGC
TTACTGCCCCGTACCGTAGGTTCCAACACATCAATAACGGCGCTGATCATGCCGGCTGTC
GTACTGGGTGCAGTATCGTTTCGCCTACGTTCTTCGCCTCACCAGACAATCCGTGAGCGAA
AACCTCCGCGCTGATTACGTTTCGAACCGCTCGAGCAAAAGGCATGTCCGGATTCAACGTG
ATGAACCGCCATGTGCTTCGAACTCACTGATTCCCGTTGCCACCTTCTTGGGCGCCGAT
CTCGGTGCACTGATGGGTGGAGCGATTGTACCGAAGGTATCTTCGGCATCAACGGTGTC
GGTGGAACGCTCTACCAGGCCATTTTGAAAGGTGAACCCACCACGGTTGTCTCCATTGTC
ACTGTGCTGGTCATCGTCTACATCATCGCCAACCTTCTCGTGGACTTGATCTACGCCGTT
CTCGATCCGAGGATCCGCTATGCC

>RXA00759-downstream

TAATAATGAATTCCACACAAACC

>RXA00760-upstream

ACCACGGTTGTCTCCATTGTCACTGTGCTGGTCATCGTCTACATCATCGCCAACCTTCTC
GTGGACTTGATCTACGCCGTTCTCGATCCGAGGATCCGCT

>RXA00760

ATGCCTAATAATGAATTCCACACAAACCACTCGTTGGGCCAAGATGATCAAACCCCAGAT
CAGGCTCATTTCTTCCCACAAGGACGAGGCGAGGCTCTAGTTTCGACCAGGTCAAGAGCAC
TTCATCGCAGCCACTGATGAAACCGGACTTGGTGCCGTCGATGCTGTTGCTGATGACTCT
GCACCAACCTCCATGTGGGGCGAAGCGTGGCGAGACCTTCGTGCTCGACCACTGTTCTGG
GTCTCTGCGGTTGATTATTTTGGCGCTTCTCCTGGCCGCGAGTTCCGCGAGCTGTTTACC
TCAACGGATCCCCAGTTCTGTGTGCTGGCAAACCTCTCTTGATGGTCCACAGTCTGGACAT
CCCTTCGGATTTCGACCGTCAAGGTTGCGATATTTTGGCTCGTACCGTCTACGGTGCTCGT
GCCTCGGTGCGCGTGGTGTGTTGACCACGTTACTGGTGCCTCATCGGTACTGTATTT
GGTGCTTTGGCTGGCTTCTTTGGTGGCATCATGGATAACCATCTCTCCGCATCACCGAC
ATGTTCTTCGCCATTCCACTGGTTCTGGCAGCCATCGTTGTGATGCAGATGTTCAAGGAA
CACCGCACCATCGTCACCGTGGTTTTGGTGCTTTGGGCTTTTCGGCTGGACCAACATTGCG
CGTATTACCCGTGGAGCGGTGATGACCGCAAAGAATGAAGAGTATGTCACCTCCGCACGT
GCGCTTGGTGCATCAAAAGCCAAGATACTGCTGTCTCACATCATGCCAAACGCCGACGA
CCCATCATTGTGTATGCAACTGTGGCACTGGGAACATTATCGTGGCAGAGGCGACGCTC
TCCTTCTGGGCATTGGCCTTCCACCATCAATTGTCTCCTGGGGTGCTGATATCGCGAAG

GCACAAACCTCCCTTCGTACCCAACCCATGGTGCTGTTCTACCCCGCAATGGCACTTGCA
CTAACCGTTTTGAGCTTCATCATGATGGGCGATGTCTCGTCCGCGACGCTCTGGATCCTAAG
TCGAGGAAGCGA

>RXA00760-downstream
TGACCACCAACATCCCACAAACC

>RXA00761-upstream
TGCTGTTCTACCCCGCAATGGCACTTGCACTAACCGTTTTGAGCTTCATCATGATGGGCG
ATGTCTCGTCCGCGACGCTCTGGATCCTAAGTCGAGGAAGCG

>RXA00761
ATGACCACCAACATCCCACAAACCCCAACCACGAGGGTGAACAGCCACTGCTCGAGCTG
AAGGATCTAAAGATTTTCCTTACCTCCTCCACCGGTGTTGTGACGCTGTCCGTGGCGCA
AACCTCACCATTATCTTGGCCAATCTGTTGCCATCGTGGGTGAATCCGGTTCAGGTAAA
TCGACCACGGCAATGTCGATCATCGGTCTGCTTCCAGGCACCGGCAAAGTGACCGAAGGT
TCCATCATGTTTGATGGCCAAGACATCACAGGCTTGAGTAACAAGCAGATGGAAAAGTAC
CGCGGTTTCAGAAATCGGACTGGTCCCCCAGGATCCGATGACCAACTTGAACCCGGTGTGG
CGCATCGGCACCCAGGTCAAGGAATCCCTCCGAGCCAACCACGTGGTTCCAGGCTCAGAG
ATGGACAAGCGCGTGGCAGAAGTTCTGGCCGAGGCAGGTCTTCTGATGCTGAGCGTFCG
GCAAAGCAGTACCCACATGAGTTCTCTGGCGGTATGCGCCACCGCGCACTGATCGCCATT
GGTTTGGCGGCACGCCCCAAGCTCTTGATCGCCGACGAGCCACCTCTGCG

>RXA00774-upstream
ATTATCGCCTTATAGTGTGGCATGCGTACTGCATATAGACAGCAATTGGATGAATTTCG
ACACAATCTAATCATTTTGTGTGATCTAACTAAGGAGTGC

>RXA00774
ATGGATAAGGCGACTGATGCCCTCCTGCGCACTTCTTTGGCATCGGCAGAAAGCGCTTTA
GGCAATGCAGAAAAGCTTGAAGAGCTTCGTACTGGATGCGAGTCTCAAGCCGTGAACTT
TTGGCGCTTGAAACTCCTGTAGCCCGTGATCTTCGCCAGGTGTCTCCTCCATCTACATC
GTGAGGAAATTACCCGTATGGGTGCTCTGGCAATGCACGTGGCTAATTCCGTGCGCCGC
CGTTACCCCGATCCGGTGATCCCGGAGGACATGCGTGGCTATTTCAAGGAGATGGCCCGC
CTCGCAGCTGACATGACAGATCATATTCGTGATCCTCATTGATCCTGAACCAGATCTT
GCCCTAGAGATGGCTAAAAGCGATGACGCGGTGGATGATCTGCATCAGCACATCATGCGT
ATTCTCACGCTGCGTCTTGGCCTCACGACACCAAGAGCGCGGTTGATTTGACGCTGCTT
TCCCGCTTCTACGAGCGTTACGCCGATCACACGGTAAACGTGGCCGCCCGTATCATTTAC
CTGTCCACCGGGCTGCACCCGGAGGAGTACATGGAAAAGCGCGAGCAACAAAGGGCCGAT
GCCGACATGGAGAAGCGCTGGGCCGAGCTGGAGCGGCAGTTCCGCAACAGCGAG

>RXA00774-downstream
TAAAAAGCTGCTTCTCGACGCTA

>RXA00775-upstream
TCATCATCGCTGTCTGAACATTGGCGCACGAATCATCTCCGCCAAGTTCTCTGTCAAGC
AATAATAATCTCAGAAAATACAACAGGAGTATCTAAAGCG

>RXA00775
ATGTGGAAGCTCAAGCTCAATGATGTCAACATCTACTACGGTGATTTCCACGCAGTGCG
AACGTGAACCTCGAGGTTCTTGACGCTCTGTACCCGATTTCATCGGACCATCCGGCTGT
GGCAAGTCCACAGTTCTCCGCTCCATCAATCGTATGCACGAGGTACCCCGAGGTGCATAC
GTCAAGGGCGAGATCCTTCTCGACGGCGAGAATCTACGGCTCCAAGATCGACCCAGTT
GCAGTCCGTAACACCATCGGCATGGTCTTCCAGAAGGCTAACCCATTCCCAACCATGTCC
ATCGAGGACAACGTGGTTGCAGGTCTGAAGCTTTCGGCGAGAAGAACAAGAAGAAGCTC
AAGGAAGTTGCTGAGAAGTCTCTTCGTGGCGCAAACCTGTGGGAAGAGGTTAAGGATCGT
CTGGACAAGCCAGGCGGCGGCTCTCCGGTGGTCAGCAGCAGCGTCTGTGCATCGCTCGC
GCGATCGCGGTTGAGCCAGAAATCCTCCTCATGGACGAGCCTTGCTCCGCGCTTGACCCA
ATCTCAACCCTGGCTGTGGAGGACCTTATCCACGAGCTGAAGGAAGAGTTACCATCGTC
ATCGTGACCCACAACATGCAGCAGGCTGCACGTGTGTCCGATCAGACCGGCTTCTACTCC
CTGGAGGCGACCGGTAGGCCAGGTCGTCTGGTTGAAATCGGACCTACCAAGAAGATCTTC

GAAAACCCAGATCAGAAGGAAACCGAAGATTACATCTCCGGCCGCTTCGGA

>RXA00775-downstream
TAAATCGAAGAATTAAAGCCACT

>RXA00776-upstream
CGTACATCTCCGCCGGCCTCGTGCTGTTTCGCCCTTACCTTCATCGTCAACGCTGGCGCTC
GCGCCATGGTTAACC GCGGAAAGTAGAAGGGGACAAAATC

>RXA00776
ATGACTAACAATGTTGTTACTCCGCGCATGGATGAGCCTTTAAAGAAGAGCTCAGCCTTC
ACCGACATCTCCTCCAGCCGTAAGACCACCAACACCGCAGCAACCGTCATCATTTATGGT
GCGATGCTCATCGCAGCTGTGCCACTGGTTTGGGTGCTGTGGACCGTGATCTCTCGAGGC
ATCGCTCCGATCCTCACTGCTGATTGGTGGTCCACCTCCAGGCTGGCGTCATGCTGATG
CTGCCAGGCGGCGGTGCAGCTCACGCCATGATCGGTACCTTCATGCAGGCGGTAGTCACC
TCGGTGATTTCCATTCCAATCGGTATCTTCACCGCAATCTACTTGGTGGAATACTCCAAC
GGTAACCGTCTCGGACGCTTGACCACCTTCATGGTTGACATCCTCACCGGTGTTTCCTTCC
ATCGTTGCGGCACTGTTTCGTGTACTCCTTGTGGATCGTGCTCTTCGGCTTCGACCGCTCC
GGCTTCGCAGTGTCCTGTCACTGGTGATTTTGATGGTTCCAGTGATCATCCGAAACACC
GAAGAAATGCTCCGCGTTGTTCTCAGGATCTGCGTGAAGCGTCCTACGCACTGGGCGTG
CCAAAGTGGAAGACCATCGCAAAGATCGTTCTCCAACCGCACTGTCCGGTATCGTCACC
GGCGTCATGCTCGCAGTCGCTCGTGTCAATGGGTGAGTCCGCACCACTTCTGGTCTTGGTT
GGTTCTCTCCAGGCCATCAACTGGAACCCATTTCGGCGGTCCGCAGGCTTCCCTTCCACTG
ATGATGCTTGATATGTACAAGGCCGGCACCGCACCAGCAACGCTGGACAAGCTGTGGGGC
GCAGCCCTCACCTGGTGCTCATCATCGCTGTCCTGAACATTGGCGCACGAATCATCTCC
GCCAAGTTCTCTGTCAAGCAA

>RXA00776-downstream
TAATAATCTCAGAAAATACAACA

>RXA00777-upstream
TTAAGTGAATCGGGCGCCCTCTCCAGCAATTGAGGGTAGGGCGCCCGATTTTACTAACA
AGCTTTTTATCAATACGCCAGTTAAGGAAATAAACCACCA

>RXA00777
ATGGCCACTAATGAGTCAGTCTCGGAGAAGCAACGCCTGGATGCAACCAGGGTGCAAGGCA
CATCCTGTAGCAGTTAATGCGAACTCCTCTCAGACCAAGCCTTCAAAGAAGATTGTCGCC
GAAGGTGGCGGAAGCGTTAAGCGTCCCGGCGATCGCATCTTCGAAGTCTATCCACCGCT
TCTGCAGCAATCATTACTGCGATAATCATTGCCATTGCGGCGTTTCCTTATCTGGCGTGCT
GTTCCCGCCTTGATGCGAAATGCTGAAGGTATTGGCGGATTCTTCACTTATTTCAGGCGCT
TGGAACACCACCGACATTGATGCAATGTACTTCGGTATTCCAAACCTGCTAGCTGCAACA
CTTCTCATCTCTGTCACTCGCACTGATCATCGCCATGCCGATTGCTCTTGGTATTGCGATC
TTCTTGTCCAATACTACCAAAGCGCCTGGTTAAGCCACTTGGCTACATGGTGGACATG
CTGGCTGTGTGCCTTCCATCGTCTACGGCCTTTGGGGCTGGCAGGTGCTCGGACCAGCT
CTGTCCGGTTTCTACACCTGGATTGAAAGCTGGGGCGGAAGCTTCTTCTCTTCGCTACT
TACCAAACTCACCTTCTTTTGCTACCGGCCGTAACATGCTCACCGGTGGCATCGTGCTC
GCAGTGATGATCCTTCCTGTTATCGAAGCAACCGCACGTGAAGTTTTCATACAGACTCCA
AAGGGCCACATTGAATCTGCTCTTGCACTTGGCGCAACCCGCTGGGAAGTCGTTTCGTTTG
ACGGTTCTCCCATTCGGAATGTCCGGCTACGTTTCCGGCGCGATGCTCGGCCTCGGCCGC
GCACTGGGTGAGACCATGGCGCTATACATGGTTGTTTCTCCATCCTCGGCGTTCGCTTC
TCGCTTTTTCGATGGCGGTACCACCTTCGCAACGGCCATCGCCAATGCCGCTCCAGAATTC
AACGACAACACCCGCGCAGGCGCGTACATCTCCGCCGGCCTCGTGCTGTTTCGCCCTTACC
TTCATCGTCAACGCTGGCGCTCGCGCCATGGTTAACC GCGGAAAG

>RXA00777-downstream
TAGAAGGGGACAAAATCATGACT

>RXA00828
GAGACCAATTTGTGGCGCGCACTGTGCGTGATGAGCTAGAAATTGGTCCGAAAATCATG
AAAGTTGATGCAAGCGAGCGCATCGAGGAGTTGCTTGATCGGTTGCGCCTCCGCCACTTA
GAAAATGCTAATCCGTTTACCTTGAGTGGTGGAGAAAAGCGCCGCTATCTGTGGCGACA

GCCTTGGTGGCAGCACCGAACTTCTCATTTTGGATGAGCCTACGTTTGGCCAAGATCCC
GAGACCTTCACAGAGCTGGTGACGATGTTGCGTGAATTAACAGACAACGGAATCAGCATT
GTGTCAGTAACCCATGATCCTGATTTTCATCGCAGCGCTGGGCGATCACCACATTGAGGTG
AGCGCGAAG

>RXA00828-downstream
TGAACCTGCTGATCAAAATTAAT

>RXA00832
ACACTGACAGCAGTGGTGTACGGGTTCTTCTGTTTCGCCAAATGGGTGCCCAAGCTGGT
GAATTTCAAGAGGTGAGGTGCGAGAAAAGGCAGACGACGACGCAAAATGGGAGGTCCCA
TTTAGAGGCTTAATCTTGATTATCACTGTGCTCCCCATCGTGTGCTGTCCCATGACATG
GCCACGGTGATGGATGAAGTCCTGGCAAGCCTTGGTGACCCGTAGCAATGGCTGGATTA
ATTATTGCCACCATTGTCTTCTTGCCAGAGACCATCACCTCCTTGAAAGCTGCGTGGACA
GGAGAGATTGAGCGAGTAAGCAACCTCGCGCATGGAGCCCAAGTATCAACGGTGGGGCTG
ACAATCCCAGCTGTTCTAGTGATCGGCGTGATCACAGGTCAAGATGTAGTTTGGGGGAG
ACCCCGATCAACTTGTGCTGCTGGGAACCACCATTGCGGTGACAGCCATTGCGTTTAGC
TCCAAGAAAGTCAGTGCTGTGCATGGCTCGGTGCTGCTCATGCTTTTCGGTGTTTACATG
ATGAGCATGTTGCGC

>RXA00832-downstream
TGATTTAGGTAGCCTGGTGGGAA

>RXA00934
CCAAGTTTTTCCATGGCGGCGCTACCCTTTGCAGGAAGGCCCATCGTTGCTACTTACCAC
GCCTCCAGTAGCGGATCGAAGCTGCTCAAGGCTTTCTTACCAGTGCTTTGCGCCATGCTG
GAGAAAGTGCGCGCAGGCATCGCCGTGTCTGAAATGGCTCGGCGCTGGCAGGTGGAGCAA
GTCGGCGGCGATCCCGTGCTGATCCCCAACGGGGTAGAGACCTCCATGTTCAAAGCCGCG
CGCCAAATCGAACC GAATGATCCTGTAGAGATCGTCTTTTGGGTGCGCTCGATGAGTCC
CGCAAAGGCCTCGACATCCTCCTGCGCGCTCTGACCAGGCTGGATCGCCCGTTTACCTGC
ACCGTCATTGGCGGCGGCACCCCGGAGAAAGTCGCCGGCATCAACTTTGTGGGCCGCGTC
AGCGATGAGGAAAAGGCAGCAATCTTAGGTGCGCGAGACATCTATGTCGACCCAAACACC
GGCGGCGAAAGCTTCGGCATCGTGCTAGTTGAAGCGATGGCCGCGGGATGCGCTGTCGTC
GCCAGCGACCTAGAAGCGTTCTCCCTGGTCACCGATTCTGAAGCCGCACAGCCAGCGGGC
GTGCTATTTAAAACCGGCTCAGACGCCGACCTAGCCAAAAAACTTCAAGCGCTTATCGAC
GACCCCTCCTCCCGTTCACGCTTATCGCCGCGGGGCTAAAGCGCGCAAACGCCTACGAC
TGGTCGACAGTATCCACCCAGGTCATGGCAGTCTATGAAACCATTGCGATCGACAAAGTG
AGGCTTGGA

>RXA00934-downstream
TGACCCTTGTTTACCTCCTCATC

>RXA00939
GGTGTCTGCTCGGTGGAGTGACCATGTCGATTGGCATGCTCGTCCACGAGGCCTCCGTC
CTGCTGGTCATCGCGATTGCGATGCTCCTGCTGCGCCCCACCCTGAAGGAAGACAAGGAC
AAGGCAGACGTCAGTACTGCTGACGCCCGCAAGGAGACGCTGAGCGCC

>RXA00939-downstream
TAACGACACAATCGCCACAGCCA

>RXA00942-upstream
CATTGACCGGCAGCTCGTCTGATTCACTGCACATCGTACATTGGACGGTGGACACGTTTC
AGAGTCCGCTGGATTTTCATCACATCGGAAGGAAGAGAATT

>RXA00942
TTGAGTACCAAAATTACCACGTCGAGGGTTTGACCTGCGCAAACGGTGTAAGTTCCGTA
GAGGATGAAATCGGCATTGTTGCGGGCACCCAGGGTGTGGATATTGATATTGAGACCGGC
CGCGTCACGGTGACTGGTGAAGGTTTCACTGACGAGGAAATCATTGAGGCTGTGCGGAAC
CGGGGCTACAAAGTTTCTGGGCGG

>RXA00942-downstream

TAGCACAATTACACATTCATCTC

>RXA00950-upstream

TCTCCGTACGCCCCACGAAGACACCTCGAAGTTCCACGCGAAATGTTTCACGTGAAACA
TCTGCTGATTTTTGTCTCCAAGTGGAGTTGAATGAGAGTT

>RXA00950

ATGAACACTCCGGCAGTTCAGGTTCAAATCTAAGTTTGAGTTTTGGGTCGTTACAGCT
GTCAACGGCCTCAGCCTCACGGTGGAGCAGGGGAGCATTACAGGCTTCCTCGGCCCAAC
GGTGCAGGAAAGTCAACAACCATCAGGGCACTCATTGGAGTGCTAAAACCCCAACAGGT
TCAGTCGCTATTCTCGGCCAAGATCCTGTTGCTCACCCGATGTCCTTCGAAGAGTTGGC
TACGTTCCAGGAGATGCCACACTGTGGGACAACCTCACTGGGGCGGAAGTTTTCAGGGCG
CTCGAATCACTCCGCAAGACTCCATCCAACCGAGCTCTAGAAAACGAGCTCATTGACGCC
TTCCAATTGGATCCCTCGAAGAAGATCCGCGAATACTCGACAGGTAACAGAAGGAAAGTC
AGTCTCATCGCGCGCTCAGTCATGAGCCGAGCTCCTCATCGTTGACGAGCCACCSCA
GGCTTGGATCCCATCATGGAGCAAGTCTTTGTACCTATGTCCGCAAGGCACGAACCAAC
GGCGCGTCCGTGTTACTCAGCAGCCACATTCTCAGTGAGGTGGAGCAGCTGTGTGATTAC
GTCACGGTCCCTAAAGAGGGGCGAGCAGTTGCATCTAATGAGGTGAGCTATCTGAGGAAG
ATCTCCGCTCACCGCATTACTGCCACGATTCGCGCGGTACCTCAACACCTTGCTGGCAGG
GGAGAAGTGGATTTTCGATGCTGGCCATCTCAGCATCACCTGCGATGCCTCCGAGGTTCC
GATATTTTGGCGATCATCATCGACGCTGGCGGCCAGGACATCATCAGCACCGCGGCGTCC
CTGGAGGAGATCTTCTTGCGTCACTATGGAGAAACCGTGAGTGGTTTCAGAAAGCAAGGCA
TCACAA

>RXA00950-downstream

TGATCCGTCTTAATCTACGTCTT

>RXA00960

CTGAAAAACGATGTTGATGTCAACGTCGCAGGCTTTGTTGTCCCACTGTGCGCCACCATC
CACCTAGCTGGATCGATGATGAAGATCGGCCCTCTTCACCTTCGCTGTTGTCTTCATGTAC
GACATGGAAGTAGGCGTCGGCCTCTCCATCGGATTCTCCTCATGCTGGGCATCACCATG
ATCGCCGCACCAGGCGTTCCCGGCGGAGCCATCATGGCAGCAACCGGCATGCTGGCCTCC
ATGCTCGGATTCAACACCGAACAAGTCGCCCTCATGATCGCCGCTTACATCGCGATTGAC
TCCTTCGGCACCGCAGCAAACGTCACCGGCGACGGCGCAATCGCAGTCATCGTGAACAAA
TTCGCCAAGGGCCAGCTGCACACCACCTCCCGAGATGAAATCGAAGAAGACGACCGCGTT
GCCTTCGACATCACTCCATCGGATGTGGAACATCACAAG

>RXA00960-downstream

TAGAAACCCGCATTTTCTGTAGT

>RXA00980-upstream

GTTGATGGACAGGCAGGTTGCTGTTGGATCTGCTGAGTTACTTGATCATGAACCAGACTC
GACCAGGATCCTGGAGCTAAATGCCGAAGGAAAGACCGCG

>RXA00980

ATGTTTGTGCGAGTGAACGGACACGCCATTGGAATCGTGGCCGTCGCCGACGCCGTTTCGT
TCAGATTCTGCCTCAGCAATCGAATCGCTGCATAAGGCGGGCATTCAAGTTGTCATGGCG
ACTGGCGACGCTCACCGCGTTGCACAAAACGTGGCCTCCAAGCTGGGAGTGGATGAAGTC
TACTCAGAGCTACTCCCTGAACAGAAATTAGAAGTGGTGCCTGATCTGCAAGCTGCCGCG
AAAACGGTCGCGATGGTGGGTGACGGAGTCAACGACACCCAGCATTGGCAGCTGCTGAT
ATCGGAGTAGCGATGGGCGTGGCAGGTTCCCTGCAGCCATTGAAACCGCTGATATCGCA
CTCATGGCGGATCGTCTCCACGGCTGGCACATGCAGTGACCTTGGCAAAACGCACCGTA
AGAACCATGCGCATCAATATTCTGATTGCGTTGGCTACCGTGATGGTGTACTAGCTGGC
GTCCTATTTGGCGGAGTTACCATGTGCGTTGGCATGCTCGTTACGAAGCAAGCGTGCTG
CTTGTTATCAGCATCGCCATGCTGTTGCTGCGTCCAACACTTAAAGAAGATGCTGCGCAA
GCAAGTGATATTAAACGCTCGGAAATACAACAGATCGCA

>RXA00980-downstream

TAACCAATGGCTGGGTACTGATG

>RXA01000

ATGTTGGCTGCCCCGCGGGGTGGGACCTTATTGGCTGCGTACCGTTTTACGGTTTCGTGTTTC
GCGGTGATTTCGTGCGTTCCCCGAAGTGGTTATCGCAATTATTTGCTAACTGTCACCGGC
CTAACTCCTTTTACTGGTGCGCTCGCATTGGGTATCTCCGGTATTGGACAACAGGCAAAG
TGGACCTATGAAGCCATTGAGTCCACTCCCACCGGCCCGTCAGAGGCAGTGCGTGACGCG
GGTGGAACTACGCCGGAGGTTCTGCGGTGGGCGTTGTGGCCACAGGTTGCGCCATCCATT
GCATCTTTTGCCCTGTACCGCTTTGAGATCAACATCCGTACCTCTGCGGTATTGGGCATC
GTTGGTGACAGGTGGTATCGGTAGTATGCTTGCCAATTACACCAACTACAGGCAGTGGGAC
ACCGTGGGCATGCTGCTCATCGTCGTGGTTGTGCAACGATGATCGTCGATCTCATCTCC
GGCACCATCCGCCGCCGCATCATGAAGGGGGCTAGTGACCGTGTCGTGGCACCAGCAAC

>RXA01000-downstream
TGACGCTCCACCAAGCATCCGCA

>RXA01002
CCCACGGAGCACGACAAGCAGATTGCTTTTCACGCGTTGGAGTCCGTGGGCATTTTGGAC
AAAGTGTTGGACCCGAGCTGGTGCTTTGTGCGGTGGACAGAAACAGCGCGTTGCTATTGCG
CGCGCCTTATCGCAAGATCCGTCTGTCTGTCATGCTGGCAGATGAGCCTGTGGCAAGCCTTGAT
CCGCCAACCGCGCATTCCTGTATGCGCGATCTAGAAAACATCAACAACGTGGAAGGCCTC
ACCGTGTTGGTGAACCTTGCACTTGATTGATTTGGCTCGTCAATACACCACAAGGCTTGTG
GGTTTTCGTGCGCGCAAGCTGGTCTATGACGGTCTATCTCTGAGGCCACCGATAAAGAC
TTTGAAGCTATCTATGGTCGCCCCATCCAGGCTAAAGACCTGCTAGGTGATCGCGCA

>RXA01002-downstream
TGACCACGCCCTTCTTCTACACTT

>RXA01003-upstream
AGCTGGTCTATGACGGTCTTATCTCTGAGGCCACCGATAAAGACTTTGAAGCTATCTATG
GTCGCCCCATCCAGGCTAAAGACCTGCTAGGTGATCGCGC

>RXA01003
ATGACCACGCCTTCTTCTACACTTATCCCACAAAAGCCTCGGGCTGGGGTAAAGACCTAT
CTCATCATCGGCGCCATCGTTGTCTTACCCTGGCAACAGCAACCCAGCGCTAGGTGGC
ATTGAGCTTGATTTGCTTCCATTGCTGCGAATTGGCGCAATGGTGCCAACAACTCCTG
CAAATGCTGCAGCCCAACTTTGCGTTCTTGCCCTCGTACGTGGCTTCCCATGTTGGAAACC
CTGCAGATGGCGCTTGTGGAGCTGTCTTGTCTGCTGCCGTATCGGTGCCTTTGACGTTG
TGGGCAGCGCAGGCAACCAACACCAGTGCGATTGGTTCGTGGCATTGTCCGCACCATCAT
AACGTGGTGCGCTCTGTCCCCGACTTGGTGTATGCCACCATCTTGGTCGCCATGGTTGGT
GTCGGCGCATTAACCTGGCATTTTGACGCTGTTTCTGTTCAACCTGGGCATCGTGGTCAAG
CTTGCTCTGAGGCCATTGATTTCCACTGAGCATCCCTATATGGAAGCAGGACGCGCAGCA
GGTGGATCACAGTTCCAAATCAACCGAGTCTCCGCGCTTCTGAAGTCATGCCGCTCTTT
GCCAACCAATGGCTCTACACCCTAGAGCTGAATGTACGCATCTCCGCCATCCTTGGCATC
GTGGGCGCAGGTGGCATCGGCAGGCTGCTTGATGAACGCCGAGCTTTCTATGCCTACGCG
GATGTTTCCGTGATCATTTCTGGAAATCCTCATCGTGGTGATTGTCATTGAAGTAATCTCC
AACGCACTTCGAAAGAGGCTGGTA

>RXA01003-downstream
TGAGCACCTTAACCTCTCACCGC

>RXA01006-upstream
GCCTTACGTGAAGGGCTTTAGCCCCGAAGTGATCGGCCGCCCGAGCTTCTATGAGACCTA
CATTGACCATTCCAGCGACCATTCAGTGAGGAGGACTAA

>RXA01006
ATGACTACCTCGCAGATTCTGCGCCGCATCGGCCAAGCCGTCTTGGTCTTGTGGTCACC
TTTACCTTGGCGTTTCATCATGCTTTCCGCCCTCCCTGGCGATGCTGTGTCCGCCCGCTAT
TCCAGCCCTGATTTGGGTCTGTACCTGAGCAGATCGCACAGATCCGTGAATCCTATGGT
GCCGATGAATCCCTGATCGCTCAGTACTTCTCCACCTTGGGTGGCTTCTTGAGGTAAC
TTCGGTTACTCCGTACAAACCGGAACCTGCCGTGGCAACCCAGCTGGCAGAAGCCCTACCA
GGCACCTTGACCTTGGCTATTTTGGCATCTTGTCTCGCAGCCATTTTGGCACTGGTTATT
TCCATTCTTGCCACCATGGATCGCTTTGCATGGATCAAGGGCATCTTCCAGGCTCTGCCT

CCATTCTTTGTGTCCCTTCCAAGTTTCTGGTTGGGCATCATCTTGATCCAGATCGTGTCC
 TTCCGCCTTGGTTGGGTCCCCGTTATTGGGACCACCCCGGCACAAGGACTGATCCTGCCG
 ACCATCACCTTGTCCATCCCAATTACCGCTCCGCTTGACAGGTGCTCATCCGCTCGATT
 GAAGAGGTCAAGGCACAACCGTTTCATCGCGGCTGTTTCGTGCTCGCGGTGCGGGTGAAATG
 TGGATCTTCTCCGCAACATCATTTCGCAACGCCCTTTTGCCAACCTGACGATTGCCGGC
 ATCTTGTTTTGGTGAAGTAGTCGGTGGGGCCGTGGTCACCGAGGCAGTGTTTCGGCCGCGCT
 GGACTTGGCCAAATGACCGTCAACGCAGTGGCCAACCGCGATATGCCAGTGATGCTTGCC
 ATCGTGGTGATCGCAGCT

>RXA01012-upstream

GACCTCATGGTGGCTGACTGTGCTGCCTGGTTTTGTTCATCATCGCCGTGGTTATGTCTGC
 CAACTACCTAAGCCGCATCATTGAGAAGGAGGCATAGAAA

>RXA01012

ATGACTACTCCCTTGTTAGAGATCAACGATCTGGTTGTCTCCTATCAAAGTCTAAAGGT
 TTGGTGCATGCTGTCAACAATGTGAGCCTGGAGGTGCACCCTGGCCAAATCACCGCGATT
 GTTGGTGAGTCCGTTCTGGTAAGTCCACCACCGCTCAGGCCGTGATTGGTTTGCTGGCT
 GATAATGCTGAAGTGGATTCTGGTCGGATTTCTTTCAACGGCCGTTCCCTTGTTGGCTTG
 AACGCACGTGAGTGGAAAAACGTTTCGCGGTACCAAAATTGGTTTGATTCCCGCAGGACCCC
 AACAACTCTCTGAACCCGGTGAAGTATATCGGCGCTTCAGTGGGGGAGGGCTTGCTATC
 CACAAGCGTGAAGCCGCGCGAGCGCAAAAAGAGTCAATTGAGCTTCTAGAGCGCGTG
 GGTATTGATAACCCAGAGGTCCGCTATGACAGTACCCGCATGAGCTGTCTGGTGGCATG
 AAGCAGCGCGCGTTGATTGCCGCTGCCATTGCACTTGAACAGAGCTGATCATTGCCGAT
 GAGCCACATCTGCGCTGGATGTGACCGTGCAGAAAATTATTCTCGATCTGCTGGAAGAC
 ATGCAGCGTGAATTGGGCATGGGTATTTTGTTCATTACTCACGATCTAGCCGTGGCAGGC
 GATCGGGCGGATCGCATCGTCTCATGCAAAAAGGCGAGGTGCGCGAAAGTGGTTACGCG
 GCTTCGGTCTTGACCGACCCCCAGCATGAGTATTCCAAGAAGTTGCTTGCCGACGCGCCC
 TCCCTCACCATCGGCGAGATCCCCACGCGAGTTCGGGCCGTAGATCCGGAGGTAGCGCAG
 GCCAAAGCCCGCTTCTGGTAGTGGATAAATTCCGCAAGGAACACCAACGAGGCAAGAA
 GGAGCATTTGTTGCCGCAAAATGATATTTCTTTCGAAGTACTGCCTGGCACCACGCATGCC
 ATCGTCTGGTGAATCCGGTCTGGTAAAACACGCTTGCCGCGCGATCGCGATGTTTAAT
 ACGCCGACCTCTGGTTCCATTTAGTAAGTGGCAAGGACATCACCAACCTGTCCAAGGCC
 CAGCAGCGGGAACGCGCCAGCAAATCCAGCTGGTGTACCAAAACCCGTATTCTTCCCTG
 GATCCTCGCCAAACCATTTGGCTCCACCATCGCGGAACCTCTGCGCAATTTACCAAGGTG
 AGCAAGCAGGAAGCCGACGAAAAGGTGGCACACTACCTGGAAGTGGTGGCGCTTGACCCG
 GCTCTTGCCACCCGTCGCCCACGTGAGCTCTCTGGTGGTCAGCGCCAGCGCGTCCGCTT
 GCTCGTGCCATGATTTTGAACCTGAATTGGTGGTTTTTCGACGAAGCCGTATCCGCGTTG
 GATGTACTGTGCGGCACAAATCCTGCGCCTGCTCGACGATCTGCAACGAGAGCTAGGC
 TTGACTTACGTGTTTATTTCCACGACCTGGCTGTGGTCCGTGAAATCTCTGACACTGTG
 TCTGTGATGAGTCGCGGCAACCAGGTGGAAGTGGAAAAACCGCAGAAGTATTTAACAAC
 CCGCAAACCGATTTCACTCGCCGACTCATCGACGCGATCCCAGGATCGCGCTATCGTGGT
 GGCGAACTCAATCTTGACTA

>RXA01012-downstream

TAGGAGCAGATCTTAAAAATGTC

>RXA01013

TTGGGCAATCCTTGGACGAGGCCTGCTGCTGTTATTTCCATCGTGGTACTCGCCGTTGCG
 GTGCTGATGGCACTTGTTTCTGGACTGTTTACCTCCCAGGATCCGTTCACTGGCGATGAT
 GTGGCGCTGCTTGGGCCAAGTGGCACCCACTGGTTTGGTACCGATTCCGTGGGACGCGAT
 CTCTACAGTCGTGTTGTTTACGGCGCGAGGGAAACCTGCTCGGTGCACTGATCGCAGTG
 CTGGTTGGTCTGATCGTGGGAACCTGATCGGACTGCTCGCAGGTGCACAGCGCGGTTGG
 GTTGACACTGTATTAATGCGTTTCGTGGATGTGCTGTTGTCCATCCCGGCACTGCTGCTC
 AGCTTACTGTGATTAATCCTTTTGGGATTTCGGCACCATGAACGCAGCGATCGCAGTCCGGT
 ATTACCTCTGTGTGACACCTTCGCGCGTCTGGCGCGTTCCAGGTGATGACTGTTGCAGGT
 TCCGATTTCTGTGAAGCTGCATACGGTTCCGGTGGCACCCAGGCGCAGGTGTTGTTCCGC
 CACATTCTGCCTAACTCTCTGACCCAGTGTTTGTCTTGCAGCACTGCAGTTCGGTTCC
 GCGATTTTGCAGCTGTCCGTGTTGGGCTTCTTGGGCTACGGCGCTCCGGCACCAACACCA
 GAGTGGGGTCTGCTGATCTCTGATGCCCGGCACTACATGGCGACCTCATGGTGGCTGACT

GTGCTGCCTGGTTTTTGTTCATCATCGCCGTGGTTATGTCTGCCAACTACCTAAGCCGCATC
ATTGAGAAGGAGGCA

>RXA01013-downstream
TAGAAAATGACTACTCCCTTGTT

>RXA01070-upstream
CAGCTTCGGTTAATTTGGTCACACTAATGCAATAAATTCCTGTCTACAGCGTTACAGTTA
ATGAATTCAATTCAACCGCTAAACGCAAGGAGTGCTACCC

>RXA01070
ATGGCTAACGCCACCGCACAGAAGGGCCGTTTCGGCCTTCCCGGCTGGATGACTGGCTTT
GGTGCCAGGTTATCGCCGGCCTCATTCTTGGTCTTATTCTCGGCCTTGTGCCCCGAGGC
ATGGACAGCGGCGCTGCAGACGGTGAAGCAAGCTGGCTTACCGGTCTTCTTAGCGGCGTC
GGTTCTGCTTATGTTTCTCTACTTAAAGTTATGGTTCCACCACTGGTGTTCGCTGCAGTG
GTTACCAGTGTGGCAAAGTTGCGCGAGGTAGCTAACGCTGCTCGCCTGGCTGTTTCCACC
TTGGTGTGGTTTCGCCATTACTGCATTCTTCTCTGTGCTCGCGGGTATCGCCGTAGCGCTG
ATTATGCAGCCTGGTGTGGATCCACTGTGACGCATCTAATGCTGCTGATCCTTCTCGC
GTGGGCAGCTGGCTGGGCTTTATCCAGTCCGTTATTCCATCAAACATTCTGGGACTTTCC
GGTTCTTACAGTGAGAACTCTGGTGTGAACCTGTCCTTCAACGTGCTGCAGATCCTGGTT
ATCTCCATTGCGATTGGTGTGTCAGCTCTGAAGGCTGGCAAGTCCGCCGAGCCTTCTTG
AAGTTCACCGAGTCCTTCTCAAGATCATCCAGATCGTGTGTTGGTGGATTATTGCGCTG
GCTCCAATTGGTTCCGCTGCGCTGATCGGTAATGCTGTTGCTACCTACGGTTGGTCTGCA
CTTGGATCCCTGGGCAAGTTGTTCTTGCGATCTACGTTGGTCTGGCAATCGTCATGTTT
GTTATCTACCCAGTCGTGCTGAAGCTCAATGGAATTCTGTTCTTGGATTCTTCAAGCGC
GTTTGGCCTGTCAAGCCTTGGCTTTGTTACCCGTTTCTCCATGGGCGTTATGCCAGTT
ACCCAGCGCTTACTGAGCAGTCTTGGGTGTTCCATCTGCGTACGCTTCTTTGCTATC
CCACTGGGTGCGACCAGCAAGATGGACGGCTGCGCTGCTGTCTACCCAGCTGTTGCCGCT
ATCTTCGTGGCACAGTTCTACGGCATTGACTTGAGCATCATGGATTACGTACTGATCATG
ATCGTCTCTGTCTGGGCTCTGCTGCAACTGCAGGCACCACTGGCGCAACCGTCATGCTG
ACCCTGACCCTATCCACCTTGGGTCTGCCACTTGCTGGTGTGGTCTGCTGCTGGCTATC
GAGCCAATCATCGACATGGGACGTACCGCAACCAACGTACCCGGTCAGGCACTGGTTCTT
GCGATCGTTGCTAAGCGCGAGGGCATTCTGGATCAGGATGTGTGGGATGCTGCTGAAAAG
GGTGGCGCTGCTATTGAAATGGCAACCGTCTCTGAGAAAGAACTGAGCCTGCAGAGGTT
CGCTCC

>RXA01070-downstream
TAAGCTCTCTTGAGTACCTGAGA

>RXA01094-upstream
GTCAGCTGACCGGGGTAGCGGGCGGTGGGCGGACAAGTCTTGCTAGATTGAAGTGCATTA
CTTGTGCGCTGACTGTTAGGTTTACGTTGTTGTGGATGTC

>RXA01094
ATGACTTTGGCCACGATTCCCTCACCACCGCAGGGTGTGTGGTACTTGGGTCCCATTCCG
ATTAGGGCCTATGCGATGTGCATCATCGCTGGCATTATTGTTGCCATTTGGCTGACGAGA
AAGCGCTACGCCGCCCGCGGTGGAAACCCTGAAATCGTCCTTGATGCAGCGATCGTGGCA
GTTCTGCGGAATCATCGGTGGACGCATTTATCACGTCATTACCGACAACCAAAAGTAC
TTCTGCGATACCTGTAAACCCGTCGACGCCTTCAAATACCAACGGTGGTCTGGGCATC
TGGGGTGCAGTGATCCTCGGTGGCCTGGCAGTGGCCGTATTCTTCCGGTACAAAAGCTT
CCTCTTGACCTTTTCGAGATGCCGTGGCACCTGCAGTTATCCTGGCGCAGGGAATTGGT
CGTCTGGGCAACTGGTTTAAACCAGGAGCTCTACGGTGCAGAACTACCGTTCCATGGGCT
TTGGAAATCTACTATCGGGTAGATGAAAATGAAAATTCGCACCGGTGACAGGAACATCC
ACCGGTGAAGTAATGGCTACTGTTTATCCAACATTCCTCTATGAACTGTTGTGGAACCTA
CTGATCTTCGCTTTGTTGATGTGGGCTGACAAGCGATTCAAGCTGGAACATGGCCGAGTA
TTTGCTCTCTACGTAGCTGGTTACACCTTGGGCCGTTTCTGGATTGAACAAATGCGCGTT
GATGAAGCCACGCTTATTGGCGGCATCCGAATCAACACCATCGTCTCCGCAGTAGTGT
GCCGGCGCGATCATCGTGTCTTCTGTTGAAGAAGGGTAGGGAACTCCCGAAGAGGTA
GATCCGACTTTTCGACGCTCTGTTGCAGCAGATGCTGTAGCTTCGCCAGATAGAAAACCC
TTGCCGAAAGCAGGGGAGGGCATTGATGGAGAAACGCCCTCAACGCGA

>RXA01094-downstream
TAGGTTTCAACCATAGGCCTGAC

>RXA01135-upstream
CATTTACTAATCTCACAAGACATCGCCTAATGAATACAGACTAGCCTATTCAAATTCAAA
GAACACTCGGTATGGCACCTGATTTAAGGATGCTGCAATC

>RXA01135
GTGACACATATCCTCTTCGACAGCAGGCGTTTTCTGCAACTGGGCGCTTTTGCGTCCTTG
AGCACCGCATTTGGCCGGAGCGGCCCGCTACGTGACGTGACACAAGCAATAATGAACCTGCG
GATAACACTCCCCTGACCATTTGGCTACGTGCCTATTGCGGGCTCGGCGCCGATTGCTATC
GCAGATGCGCTAGGGCTGTTTAAGAAACACGGCGTGAATGTCACGTTGAAGAAGTACTCA
GGCTGGTCCGACCTGTGGACCGCTATGCAACAGAGCAGCTTGATGTTGCGCACATGCTG
TCGCCGATGACTGTGGCGATTAAT

>RXA01141
GTCAATTCAAGCGGCGGATCTTAAAGGCATGGTGCTGGGAATTCCTTTTGAATATTCAGTC
CATGCGCTGCTCCTGCGGATTATCTCGTCTCAAACGCAGTTGATCCCATCGCCGATCTT
GAGCTTCGCCTGCTCCGACCTGCCGATATGGTGCACAAATTGACAGTTGAGGGCATCGAT
GGATTCATTGGGCTTGGGCCGTTTAATGAACGCGCCATCAGCAATGGCTCCGGCCCGGATT
TGGCTGCTGACCAAACAACGTGTGGGACAAACATCCATGCTGCGCCGTGGCGATGGCCAAA
GAGTGGAAAGCTGAACACCCACGGCGGCTCAGGGTGTGCTTAATGCGCTGGAGGAAGCC
TCCGCAATTTTGAAGCAATCCGGCACAATTTGATTCTCGGCACGCACGCTGTGCGAGGAA
AAATACCTCAACCAGCCTGCCACGTTGCTGGATGGACCGTCG

>RXA01141-downstream
TAATCATCGGCATCACCGGCTTA

>RXA01142
ACCCGCACCCACCTCGAACAAGTAGGCCTCACCGACGCCGCCGAACGGCGCCCCGCCCCG
CTCTCCGGCGGCATGCAACAGCGAGTCGGCATCGCACGCGCCTTCGCCATCGACCCACCA
ATCATGCTTCTCGACGAACCTTCGGAGCCCTCGACGCCCTCACCCGCCGCGAAGTCCAG
CTCCAACTACTCAACATTTGGGAAGCCTCCCGCCGCACCGTCGTGATGGTCAACCCACGAC
GTCGACGAGGCCATCCTGCTCTCCGACCGAGTTCTCGTGATGTCCAAGAGCCCCGAAGCC
ACCATCATCACCGATATTCAGTGAATCTTCCCCGCCCGAGACACGAGCTGAGTGAAGAC
GCTTCTGTTGAAGCCGAGACCACAGCCCTGCGTAAGCGGATGCTGCATCTGCTGGAGCAC

>RXA01142-downstream
TAGTTTCTAACACGTCTTTTAAA

>RXA01164-upstream
GCCGATCGTGATTGATGAAGACGAGATCCAAGCCTGGACTTCTGATCTCAAACCTGAAGA
TTTCACCAAAGGTAAAGATGAATCCGACGGTGAGAAATAA

>RXA01164
GTGACACTGTTTGTTTCGGCTCGCCCTTGCTGCTGTGGGCGGGCTTTTTGTCTTTGCTTCC
AATGAACCGATCGGCTGGTTTGTGCGGGAATTGTTGGCACTGCATTATTTTTTATCTCC
CTTGCGCCGTGGGATCTGGGAGTTCCCCAAAAGCGGCGGAAGAAGAATGAGCCAGTCCCA
TTTTTGAACAGATGTCCACGGGCCCAACTGTTGTACAGGGCATGCTTTTAGGTTTTGTC
CATGGCCTGGTGACATAATTTGCAGCTGTTGCCGTGGATCGGTGAGTTTGTGGCTCACTG
CCTTATGTCGCGTTGTCAGTTGTCGAGGCGCTTTATTCCATTGCTCTTGGTGCTTTCCGGC
GTGCTCATTGCGCGTTGGAGGGACTGGAAGGTTCTCCTGTTTCCGGCGATGTATGTGGCT
GTGGAGTATCTAAGAAGCTCGTGGCCATTTGATGGATTTCGCGTGGGTTTCGCTGGCATGG
GGTCAAATTAACGGTCCGTGGCTAATCTCGCAGCGCTTGGTGGGGTAGCGTTTGTCACT
TTTTCCACGGTGCTGGCTGCCGTGGGTGTGGCCATGGTGATTATTTCCAAGAAGCGACTG
GCCGGCGCAATCATCACCGCGAGTGTGATTGCTATCGGCGCGGTGTCATCCCTGTACGTT
GACCGCAATGGCAGCAGCGATGAAAGCATCGAAGTAGCCGCAATTCAGGGCAATGTGCCT
CGGATGGGATTGGACTTCAATGCACAGCGCGCGCGGTGCTGGCGAATCACGCACGGGAA
ACCCCTCAAGCTGGATGAACAAGTGGATTTGGTGATCTGGCCGGAGAATTCTCAGACGTC
AACCCATTTTCCGATGCACAAGCAAGAGCCATTATCGATGGAGCAGTGAACATGTTGAG
GCACCTATTTTGGTGGGCACGATCACCGTCGATGAGGTTGGTCCACGCAACACCATGCAG

GTATTTGATCCTGTTGAAGGTGCCGCGGAGTACCACAATAAGAAGTTCTTGCAGCCGTTT
 GGTGAATACATGCCGTTTCGCGAATTCCTGAGAATTTTCTCGCCCTACGTTGATTCCGCT
 GGAAACTTCCAGCCCGGTGATGGCACC GGCGTAGTGGAGATGAATGCTGCGAACTTAGGC
 CGCGCTGTGACAGTGGGCGTGATGACGTGTTACGAGGTTCATCTTGCACCGTGCTGGCCGC
 GACGCCATCGCCAATGGGGCTGAATTTTGGACCACGCCACCAACAACGCCACCTTCGGA
 TTCACGGACATGACGTATCAGCAATTAGCAATGAGCAGGATGCGTGCCATCGAATTTGAT
 AGGGCGGTGGTTGTTGCAGCTACATCGGGTGTTCGGCTATCGTCAACCCTGATGGAAGC
 ATTTCCCAAACACCCGAATTTTGGAGCCGCCACCTTGACGGAATCCATTCCACTCAAG
 GACACTGTCAACATCGCAGCGCGGGTTGGTTTCTATGTTGAATTACTGTTGGTTATCATT
 GGTGTATTAGCTGGACTATTGCCATTTCGAATGAATAGCCGTTCAAAGTCTGCGAAAGGT
 TCCGCTCGGCCCGCA

>RXA01168

CGCACCGCAACCCCTGACGTTACGTACTCATCGTGGACGACAACAGCCCAGACGGCACC
 GGCGAGCGCGCAGACAAGCTTGCTGCTGACGACGACCACATTTTGTCTCCACCGCGAA
 GGCAAAGGCGGCCTGTGCGCAGAGTACATGGCTGGCTTCCAGTGGGGCCTGGAGCGCGAC
 TACCAGGTCTGTGCGAAATGGACGCCGACGGCTCCACGACCCAGAACAGCTGCACCTG
 CTGCTCGCTGAGATCACCATGGCGTGACCTGGTCATCGGCTCGCGCTACGTGCCAGGC
 GGCCGCGTAGTCAACTGGCCCAAGAACCGTTGGCTCTTGTCCAAGGGCGGCAACGTCTAC
 ATCAGCGTCGCGCTCGGCGCCGGCTTGACCGATATGACCGCAGGGTACCGCGCTTTTCGA
 CGTGAAGTGCTAGAAGCACTGCCGCTTGATGAGCTCTCCAACGCTGGGTACATTTTCCAA
 GTTGAGATTGCCTACCGTGCAAGCTTGAAGCCGATTTCGATGTTTCGTGAAGTTCCCATCACT
 TTCACCGAGCGTGAGATCGGCGTCAAGCTGGACGGCAGCTTTGTCAAGGATTCCCTG
 CTCGAGGTAACCAAGTGGGGCCTCAAGCACCGCGGTGGCCAGGCCAAGGAACTGTCCAAG
 GAAATGGTCGGCCTGCTGAACCTATGAGTGGAAGCACTTCAAAAAGCGCAACACCTGGCTC

>RXA01168-downstream

TAAACTGCTTGCCGGTTAGTGAA

>RXA01185-upstream

TCAGCTGGTAGCGTCGCATGTATTATTGGTGCTTTTCACTAATAGCAATGCACTAACGCA
 CATAGCCGCCGACACGTGAATCGAAAGAAGTTCATCTCCG

>RXA01185

ATGACTGATCCTGAAAACCTCGCAAGGAACCCACAGATTTGTCCGACTGATCCGACTACG
 CAAGCATTAGCAGTTCGGGGCTTAACCAAGTCCCTATGGTGATGCAACAGTAGTGAACAAT
 ATCAATCTGGACATCCCCAAGGAGCCATTTACGGCATCGTTGGACCTAATGGTGCAAGT
 AAAACCACCATGCTGTCCATGGCAACGGGTTTACTGAGGCCGAATAAAGGCACCGCGTGG
 ATTTCCGGGTTTCAATGTGTGGGAAGAGCCAAACGATGCAAAACGAAGCATGGGATTGTTG
 GCAGATGGCTTGCCCATCTTTGATCGCTTGACTGGCAAGAAGTGTACATATGTCGGG
 GCATTGCGTGAGTTGGATGAAGGCATTGTTGATCAACGTAGTGAGGAATTGCTGGAGGCC
 CTCGGGCTTAAAGAAGCAGCGGGCAAGAGAGTGTGTCGACTATTCCGCCGGCATGACGAAG
 AAGATTCTTTTGGCCCAGGCCCTCATTCACAATCCGAAAGTGTCTATCCTTGATGAACCT
 TTGGAAGCGGTTGATCCGGTGTCTGGTCTGTTGATTGAGCAGATTTTGAAGAAGTTTGC
 CAAACGGGTGGAACCGTCGTTTGTAGTTCGCATGTGATGAATTGGTTGAGGGGTTGTGC
 GATCACGTTGCCATCATCAACAGGGGAGTGGTGGAGATTGCCGGACATGTGAATGAGGTT
 CGTCGGGCGAGATCTTACCGGATGTCCTTCGTTAATGCGGTTGAAGGCGCTGCTCTCAAG
 AGGGGTCACTATCTTGGTTGGGTGCGTCCGAAGGCCATAGCGAAGGCCAAAATCAGAACG
 AGGATCGGGCTGAGTAAA

>RXA01185-downstream

TGACTAAAACACTTCTGAAACTA

>RXA01188-upstream

AAACAGTTAGAAGCACCTAAACAGTTTTTCCGATAACTGTTGTGATTTTGTGACCGCCTG
 GCTTTGTAGTTTTCCCTCCGGTGTCGAAGATGAATATGAC

>RXA01188

ATGATGAATGGCGTGGTACAGCCTCAGGAACATCTCGATGCAACGTTGATTGCTGCAGAC
 TTCCACGGCAACCCCGAAAACCTCTGGTGACCGCAAAGAGCGCCTGAATTTTCAAGGTTGG
 AAGTATGCCCTTAATCGCACGGTCAGGGATGTTTTTCCAGATGGCCTGCTCGATTGGCG

GCCTTGTTGACGTTCTTTTCCATTCTGTGTCGATCGCCCCCTGCAGTGCTGCTGGGCTATTTCG
 GTGATCACGATTTTTCTGGCCAGTGAATCCACCGAAATCCTCAACCTTGTCGCGCATGAG
 GTAAATCAGTACGTTCCGGAAGATCAATCCCATGTTGTCAACGGCGTGATTGATTTCGATC
 GCAGGCTCGGCAGCTGCAGGTGAGTGGTGTGCGGGTGGTGTGATCACGGCATTTGTGG
 ACATCTTCGGCATATGTGCGCGCTTTTTCCAGATGTGCCAACGCTGTTTATGGCCGAAGC
 GAAGGCCGACACATTGATCAAACGCTGGGCAATGCTGCTTTTCCCTCAACCTTGCTTTGCTG
 CTTGGAATCATCATCATTTTTGGTCTCCTGGGTGCTCAACGAGACCTTGGTGATGGGAATT
 TTCGCCCCCATCGCGGAACCACTTCATCTCACGAATGTGCTCAGCTTCCTCACGGACCGG
 TTCATGCCGATCTGGATCTGGGTGCGGTTCCAGTGATTGTGGGGGTGCTCATCATGTTT
 GTGGCCACGCTGTATTACTGGGCCCCGAACGCCCCGCGCTGGAAGTTTCGCTGGCTCAGC
 CTCGGATCATTTCTGGCGATCGTTGGCATCCTGCTCGCAGGCGTGCGCTTGAATTTCTAC
 TTCACGCTGTTTCGCGCTTTTAGTTCTACGGCGCGGTGGGTTCGCTGCTCGCGGTTTTT
 ATTGCGCTGTGGGTGTTCAACATTTGCTTAATCATCGGCCTGAAAATCGACGTGGAGATC
 AGCCGCGCAAGCAACTGCAGGCAGGAATGCCGGCGGAGGATTACAGTTTAGTGCCACCA
 CGCTCTATCGAGAAGGTGGCGAAAATGAAGCAGCGCCAGCAGCGCTTGATGGATCAGGCT
 GCGGCGATCCGGGAGGAAAGCAAT

>RXA01188-downstream
 TAAAAAATTGCTTATCGACGTCC

>RXA01245
 GCCTCCTGGGTCAACACCCTGGGGCTGGGCGGGTTCACCTAGATTTCTGGTGGGAAGT
 GCCCTGCTGGTGACCATAATGCTGTTGGGCCACTGGCTGGAGATGCGCGCTCTTGGTGCA
 GCCTCCTCCGCGCTTGACGCGCTGGCAGCGCTCCTGCCCAGTGAAGCCGAGAAGGTCGTC
 GACGGGACCAACCGCACCGTAGCGATCTCAGAGCTGGCCGTCGACGATGTCGTGCTGGTC
 CGAGCAGGTGCCCGCTCCCGGCCGACGGGACCATCATGGACGGAGCGGCCGAATTCGAT
 GAGGCCATGATCACCGGCGAATCCCGACCCGCTACCGGGGATACCGGTGAGACCGTGGTG
 GCCGGCACCGTGGCCACCGACAACACCGTCCGTATCCGGGTGGAGGCCACCGGTGGGGAC
 ACCGCCCTGGCAGGCATCCAGCGCATGGTCGCCGACGCCAGGCCTCCTCCTCCCGGGCC
 CAGGCCCTGGCCGATCGAGCCGACGCTTACTGTTCTGGTTCGCCCTGATCACGGCCCTG
 ATCACCGCCGTGGTCTGGACCATCATCGGCAGCCCCGACGATGCCGTGGTCCGCGCGGTG
 ACCGTGCTGATCATCGCCTGCCCGCACGCCCTGGGCCTGGCCATCCCGCTGGTTCATCGCG
 ATCTCCTCCGAGCGCGCCGCGAAATCCGGGGTGGTTCATCAAGGACCGCATGGCACTCGAG
 CACATGCGCACCATCGACGTCGTCTTGTTCGATAAGACCGGCACCCTGACCGAAGGCGCA
 CACGCCGTACCGGCGTGGTCCCGGCCACGGGTATCGCCGAGGGTGAGCTGCTGGCCCTG
 GCCGCCGCCGCTGAGGCCGATAGTGAGCACCCCGTGGCCCGCGCGATCGTGACTGCCGCG
 GCCGCACACCCGGAGGCCCTCGCAGCGTCAGCTGCGCGCAACCGGTTTACCGCCGCCCTCC
 GGCCGCGGGATCCGGGCCACCGTCGACGGTGCCGAAATCCTCGTGGGCGGGCCGAACATG
 CTACGCGAGTTCAATCTGACCACCCCGGTGAGCTCGCCGACATCACCGGTTCTTGGGCA
 CAGCGAGGTGCCGAGTGCTACATGTCGTCCGCGACGGTGAGATCATCGGTGCGGTGGCA
 GTGGAGGACAAAAATCCGCCCGAATCCCGCGCGGGGTACGCGCCCTGCAGGCCCGCGGG
 GTGAAGGTGGCGATGATCACCGGTGACGCCACCCAGGTGCGCCAGGCAGTGGGCAAGGAT
 CTGGGGATCGATGAGGTCTTCGCCGAGGTTCTGCCGAGGACAAGGACACCAAGGTCACC
 CAGCTGCAGGAGCGCGGTCTGAGCGTGGCCATGGTCCGCGACGGTGTCAATGACGCCCCG
 GCCCTGGCCCCGGGCCGAGGTCCGTATTGCGATTGGCGCGGGTACAGATGTGGCGATGGAG
 TCCGCCGGGGTGGTCTGGCCAGTGATGATCCCCGGGCCGTGCTGTCGATGATCGAGCTC
 TCCCATGCCAGCTACCGCAAGATGGTCCAGAACCTGGTCTGGGCGACCGGGTACAACATC
 GTGGCCGTTCCGCTGGCCGCCGGTGTGCTCGCCCTATCGGTGTGCTGCTTCCCCCGGCG
 GCGGCCGCCATCTTGATGTCCCTGTCCACGATCATCGTCGCCCTCAACGCCCGAGCTGCTA
 CGCCGGATCGACCTGGACCCGGCTCACCTAGCTCCGACCGACGGGAAGGAGGAGAAGGCT
 GCTGTGAGCTCTGCAGCCCCCGTCCGC

>RXA01245-downstream
 TGACTTTCAATGCTTCATGGACT

>RXA01247-upstream
 TCCGATGACCACCCGACTTCCCCCTTGCTGCCGCTGGCCTCCGACGGTTGTGGATGCTG
 CGCGCCCTCTACACCGTCCGCGACCGTCTCCGCCTCGGCC

>RXA01247
 GTGGCCCGGCAACCGACGCAACACCTGAAGGTCCACACCTACCAGGTCACAGGCATG

ACCTGCGGACACTGCGCCGACAACGTACCGAGGCGGTGAGCGCTCTGCCCCAGGTCGAC
GACGTCCAGGTCGACCTCATCGCCGGTGGGGTCTCCATCGTCACGGTCACGGGTTCGGTG
CCCCTGGAACCGTCCACCGGGCAATTGAGGAGACCGGCTACACCGTCTTGTC

>RXA01247-downstream
TGATCGATTACCCATCATCTCG

>RXA01285
CCACAGACCTCCATCGCCCCAGAAGGCATCCGGGTTTACGATCTCATCGCGCGCGGGCGC
GCTCCCTACCAAAGCCTCATACAACAATGGCGCACCTCCGACGAAGACGCCGTGCGCAA
GCGCTCGCCTCCACGAATCTACCGAATTGCGAGTCGCCTCGTCGATGAACCTCTCCGGT
GGCCAGCGCCAACGAGTGTGGGTGGCCATGTTGCTCGCCAGCAAACACCGATCATGCTT
CTCGACGAGCCACACCTTCCTCGACATCGCCACCAATACGAACCTCTTGAATTGCTG
CGCGCATTCACGAGGCGGGGAAAACCTGTGGTCACTGTGCTTCACGATCTCAACCAAGCC
GCCCCGTACGCCGACCACCTCATCGTGATGAAAGATGGGCACGTACATGCCACGGGCACA
CCGGAGGAAGTCTTAACCTGCCGAGATGGTTCAAGGAGTTTTTGGCCTGCCCTGCATCATC
TCCCCAGACCCCGTCACAGGAACCCCCACCGTCGTTCCCCCTCAGTCGGTCTCGCGCAGGA
GCT

>RXA01285-downstream
TAAGTAGCTACCCCTCCAACGGA

>RXA01289-upstream
CTCACCTAAGATGTTCTAAGCGTTTTAGTTTTAGCTAGTTTTAAGGACTTTTCGATGTCTC
ATACTTTTCTTTCCCCCTCGATCTTTAGGAGTCACGCGAT

>RXA01289
ATGACGGCGGTGGCGGTAGAGAAGCAGAAGGAGACGTCGATAAGCAAAAACCTCGGCAGG
CGCCGAGCGCTGGGCATTCTCGGAATCGTCGTGGCACTGGGTGCGCTTATTGTTTTAAGT
ATTGCTGTGGGTGCGAACCACCTTTCTTTTAGCTCCGTATGGCAGGGTTTTACCGCACAC
GACAGCTCTGAGGCGTCGATTATCGTGTGGTCAATGCGTATTCGCGCACGCTGGTGGGC
ATCGTGACTGGCGCTGCTTTTGGTGTGGCGGGTGCTTTAATTCAAGCGCTGACGCGCAAC
CCGCTTGCCGATCCCGGAATTTTGGGAGTTAACGCGGGTGACAGGTTTCGCAGTGACCGTA
GGTGTGCGGATTTTTCGGACTCAGCAGCGTGACGGGCTACATCTGGTTCGCATTCCTGGGC
GCTGCCGCCGCTACCCTGCTGGTGTATTTTATTGGTGGCAGCACCAGCGGCAGCGTTAAT
CCTGTTGCTCTGGTCCCTCGCCGGCGTGTCTGCGCCGCGTGCTTGGTGGCGTCACGAGC
TTCTCACAACGATGATCCTGAGACTTTTGAAAGCATCCGCAATTGGAATCTTGGTTCT
GTTGCACGCACCGACCTCAGCGACACCATGACCGTATTGCCATTCTGGCAGTCGGACTG
GCCATCGCGCTCCTGCTGTGCGGAGCACTGAACCTCCATTGCGCTTGGCGATGACCTTGCT
GCATCCCTGGGCACCAAAGTGATGCGCACCGCGTGCTCGGCATCATTTTCAGTACCTTG
TTGGCCGGCGCGCGACCGCCTTACTGGTGGTATCGGCTTCGTAGGCCTTATGGTTCCC
CACGTTGTGCGCTGGGTAGTTGGCCCCGATCAACGATGGATCATCACCTTCAGCGCCCTG
TGCGCCCCCTGTTCTTGTACTCGGCGCAGACATTTTGGGACGCATCATCGCCCGCCCCGGC
GAAATTGAAGTAGGCATTGTTACCGCAGTCATCGGCGCACCTGTCCTGATCGCACTAGTT
CGACGGAGGAAAGCCAGTGGTCTT

>RXA01289-downstream
TAATATCAAATCTAGAACTGATG

>RXA01290-upstream
GGACGCATCATCGCCGCCCCGGCGAAATTGAAGTAGGCATTGTTACCGCAGTCATCGGC
GCACCTGTCTGATCGCACTAGTTTCGACGGAGGAAAGCCA

>RXA01290
GTGGTCTTTAATATCAAATCTAGAACTGATGAAACTCCTGTTGCTGCGTCTGAGCCGGTG
GAATCCACTAGACCTGTGTCTGAAGCTTCGACAAGCCCTGCGCTTAACCCCGGCTACCAC
GCAGTTTTCAGTGCAGAGGCGCCGTTCTCTTTCCGCATCCAGCCCGCCTCATGGTGGTT
AGCCTTATCCTTTTCGCCATCGCGCTATGCAGCGCCACATGGGCTATCACGATGGGCGAT
TACCCACTGTCTTTGGGGCAGGTGATTAATGCACTTGCTGGCACCGGCGAGAAATTCCAG
TTGTTGGTGGTGGCGGAATGGCGTCTACCTGTAGCCATTGCTGCTGTTGTCTTCGGCGCG

CTGCTTGGCATAGGTGGAGCGATTTTCCAGTCGATTACTCGAAACCCGTTGGGTTACCT
 GACGTGATTGGTTTCGATGCAGGTTCTTACACGGCGGTGGTTCTTGTCATTTTGGTCCTC
 GGCAACACTCACTACTGGAGCATCGCTTTTCGCTGCCATCGTCGGTGGCATTGTTACCGCC
 TTTGCCGTGTATGTCCTGGCGTGGCGTAAAGGTGTGCAAGGTTTCCGCTTGATCATCGTG
 GGCATCGGTGTCTCGGCCATGCTCAGTTCCGTTAACGCGTATCTAATCACCCGCGCCGAT
 GTGGAAGACGCCATGGTTGTGGGCTTCTGGAGTGCCGGTTCCATCAACCGCATTACCTGG
 CAATCTCTGCTCCCCTCTCTGGTGATCGCTGCTGTTCATCATCGTGGCCGCCATTGTGCTG
 GCAAGGTCACTGCGTTTCATGGAATGGGCGATGACGTAGCCACCACCCTCGGTGTGAAA
 ACAAACCTCCACCCGCTTGGCACTCATCGTTGTGCGGCGTTGCTACCTCCGCGTTGGTTACA
 GCAGCTGCCGGACCGATCTCCTTCATCGCGTTGGTTGCCCCACAGCTGGCACGTCGCCCTC
 ACTAAAACCCCTGGTGTCAGCCTGGTTGCTGCCGCTGCAATGGGTTCCGCACTGCTCAGC
 TGGCTCACCTCCTTTCCCTGATTATCAGCTCCTTCTACCGCACCATCCCGGTTGGCCTG
 TTGACTGTATCCATCGGTGGTTGCTACATGATCTGGCTTCTGCTGCGCGAAACCCGCCG
 CAATACCGCACCCGCCACCATCCGA

>RXA01290-downstream
 TAGTTCTTTTAAGGATCCCTCAT

>RXA01297-upstream
 TCCTGTTGCTGCTGATTATCACTGTTATCCAGGTTTCGATACATGGATAAGGAGAACAAAGC
 AGAAATGATCTCGACTGATAGAAACGTTTTGGTCAAAATC

>RXA01297
 ATGGGCTATGTCGGCATGGTTCTTGCCATCTTGTTTATTGGCCTTCCGCTGGTATTTATT
 GTGCTGACTAGCTTCAAGCAGCAGTCAGAGATTTACACCCAGCCGGTCACGTGGTTCCCT
 TCGGAATTTAATTTTCGATAACTATGCAAATGTTTTTCGAGCGGGTTCCGTTCTGAACTAC
 TTCCGCAACTCGATCATCATCACGGTTATTTTGTGTCTGGTGAAGATTATCTTGGGTGTG
 ATCTCTGCATATGCGTTGTCGATTTTGGCGTTCCCGGGTCGAAACCTTGTGTTCTTGCTG
 GTTATCTCCGCGCTGATGGTGCCTTCCGAAGTGAAGTATTTTCCAACATATGCGTTGGTC
 AGTCAGCTTGGTTGGCGCGATACCTACCAGGGCATCATCGTTCCGCTAGCGGGTATTGCT
 TTCGGAACGTTTCTCATGCGTAACCACTTCATGTCTATTCTTCTGAGCTCATTGAAGCT
 GCGCGAATGGATCACTGTGGACACTTCAGGTTGCTCTGGAAGGTTTGTCTCCAATCTCT
 ATGCCTACGTTGGTGGCGTTCTCCATGATCACCGTGGTGAATGAATGGAACCAATACCTG
 TGGCCTTTTCTGATGGCAGAAACCGATAATTTCAGCAACTCTGCCATTGGTTTGACCATG
 CTTCAAAACAATGAGGGTGTCTCCAACCTGGGGACCTGTCATGGCCGCAACGATCATGACC
 ATGTTGCCTGTGCTTGTGATGTTCTTGGCACTGCAGGAGTACATGATCAAGGGACTTATC
 TCCGGCGCCGTCAGGGC

>RXA01297-downstream
 TAAAAACTTCTCGCTAAAAACTT

>RXA01298
 TTCGTGTGGAAGAACTTGGGCTACTCCTTTGTTATCTACCTGGCTGCATTGCAGGGGGCTA
 AACAAGGATTTGTCTGAGGCCGCACCGGTGGATGGCGCGAGCGGTGGACACGTTTTTGG
 AAGGTTACTCTTCCGAGCTTCGCCCCAACCACGTTCTTCTTTCTATTACTGTCACGCTG
 AACTCGGTTTCAAGGTTCTCGACATCATTCACACCATGACTCGTGGTGGCCCCCTTGGGTAAC
 GGTACGACCACCTTGGTTTACCAGGTGTACACCGAGACTTTACCAACTATCGCGCGGGA
 TATGGTGAACAATCGCAACGATTTTGTTCCTGTTGCTGCTGATTATCACTGTTATCCAG
 GTTCGATACATGGATAAGGAGAACAAGCAGAAA

>RXA01298-downstream
 TGATCTCGACTGATAGAAACGTT

>RXA01303-upstream
 AACATGCGGGCGCAGGTGAGAGCTGTTATCTTAGTACTTATCACAGCCATAGGGCGGGCT
 TGACGGAAAGCCTTTCCGCGTAACCATGAAGAGGCATCAC

>RXA01303
 GTGACACAACCTCAACACCAAAGGCGTTGTTCTGCAAGGGTGGGATCCAGAAGATCCTGAA
 CATTGGGACTCGAAAATTGCATGGCGAACCCTGTGGATTACCACCTTCTCCATGATTATT

GGGTTCTGCGTGTGGTATTTGGTTTCTGCCATCGCTCCCCTACTCAATCGAATTGGATT
 GATCTCTCAGCAGGTCAGCTTTATTGGCTCGCATCTATCCCCGGTTTGGCCGGCGGATTA
 ATCCGATTGATTTACATGTTCTTCCACCGATTCTTGGAACCCGCAAATTGGTCGGAATT
 TCCTCCGGTCTATTTTGGATCCCCATGTTTGGGTGGTTTCTGGCTGTCCAAGATTCAAGC
 ACTCCCTACTGGTGGCTTCTCACACTCGCTGCACTCACTGGCATTGGTGGTGGCGTGTTC
 TCTGGATATATGCCGTCCACGGGATACTTCTTCCCCAAGGCAAAATCGGGCACTGCGCTG
 GGCATTACAGGCAGGTATCGGCAACCTCGGCGTCTCGATAATTCAAGTTCATGGGCCCATGG
 GTCATGGGTTTTCGGTCTGTGGGCATTGGTTTCTCACCCCGCAGCGCACCATTTGAAGGC
 ACCACGGTGTGTGTGCACAATGCTGCGATTGTGTTGGTCCCGTGGACTATTCTCGCGGCC
 GTTTTATCCTTCTGTTTCTTAAAGATGTCCAGTCACCGCAAATTTCCGGCAACAGATC
 GATATCTTTGGCAACAAGAACACATGGATTTTGTCCATTATCTACTTGATGACATTCGGT
 GCCTTCGCGGGTTTTCGCCGCGCAGTTCCGGTCTGATCATCAACAACAATTCGGCATCGCT
 TCCCCGATGGCAGAGACTTATCCAGCTGAGATGCTTCACGCCGGTGTACGTTTCGCGTTT
 CTTGGACCTTTGATTGGTGTCTTGGTGCCTGCTGATGGGGTCCACTGTGTGACAGATTC
 GGTGGAGCTATCTGGACCTTTGTCCGGTGGCATCGGAATGACTATCGCCACTGCAGCTGCC
 GCAATCTTCTAAGCAGAGCGGAGACACCTGATGATTTCTGGCCATTCTGTGGTCCATG
 CTTGCCCTGTTCTTCTTCCCGGTCTGGGCAATGCTGGCACCTTCAAACAAATGCCCATG
 ATTTTGCCTAAACGCCAAGCAGGTGGCGTGATCGGCTGGACCGGTGCCATTGGTGCCTTC
 GGCCCTTCATTGTGCGGTGTCTTGTCTCCTTCACTCCAATGTCGCGTTCCTTCTGGGGC
 TGCGTGGTGTCTTCATCATCGCCACCGCTTTGACCTGGATCTACTACGCCCGCCGAAC
 GCTCCATTCCCGGA

>RXA01303-downstream
 TAAACCGAAAGGCCAATCCATGA

>RXA01323-upstream
 CACGTGGTTTACGCCAGGCATGTTCCCGCGAAGGGTTGACCCATACCCCTAGGGGGTATA
 CAGTGAGTCATGTAAACATACTCGCAGAAGGAGCGATCCC

>RXA01323
 ATGGCTCAGACACCCGCCAAAATCCCGCGGCACTGAATTTCAATTGACGTGACCTCGGC
 GTTACCGGCATGACCTGCACTTCTTGCTCCGCCCCGCTCGAGCGCAAACCTGAACAAGCTC
 GACGGCGTTGAAGCAACCGTCAACTACGCGACGGAATCCGCACAGGTCAGTACGACCCC
 TCAAAGGTCAGCCCTGAACAGCTGATTAAGACTGTTGAGGACACCGGCTACGGTGTCTTC
 ACGATGGCTTCCGCAGCTGCCGAATCAGAAGAGGACAACGCTCCAGCTGACAGCGGCCAG
 TCCCGCATCGACGCAGCTCGCGACCACGAAGCAGCCGACCTGAAACACCGCGTGATCGTC
 TCTGCACTGTTGTGAGTTCCTGTGGTTTTGGTCAGCATGATCCCGGCGTGCAATTC AAC
 AACTGGCAGTGGGCCGTACTCACTTTGGTCACCCCGATTTTCTTCTGGGGCGGTTACCG
 TTCCACAAGGCAACGTGGGCAAACCTGAAGCGCGGTTCTTCAACATGAACACCCTGGTT
 TCACTCGGCACGTCCGCTGCTGACCTGTGGTCCCTGTGGGCTTTGTTCAATTGAAAATGCT
 GGTACCCCTGGCATGAAGATGGAGATGCACCTGCTGCCGTGGCCTCCACGATGGATGAG
 ATTTACCTCGAAACCGTCGCGTCTGTTATTACGTTCTGCTGCTTGGACGCTGGTTGAG
 ACAAAAGCTAAGGGCCAATCTTCGGAAGCTCTGCGCAAGCTGCTGGACATGGGGCCCAA
 GATGCAGTCGTCTTACGTGACGGCGCCGAAGTCCGCGTTCTGTGAATCAGCTTAAACTC
 GGCGACGTTTTTCATCACCCGCCCGCGGAGAAAATCGCCACCGACGGTGAAGTCGACGAA
 GGTTCCTCCGCACTGACGAATCCATGCTCACCGGCGAATCCATCCCCGTTGAAGTCACC
 AAGGGCTCCAAAGTTACCGGCGCAACGCTGAACACTTCCGGCCGCTCATGGTGAAAGTA
 ACCCGCATCGGCGCCGACACCACCTGTGCAAAATGGCTAAACTGGTCACGGACGCACAG
 TCCAAAAGGCCCTGTCCAGCGTCTTGTGACCAAATCTCGCAGGTTTTCTGTTCCCGTT
 GTCATCGTAATTGCTATTGCGACGCTGATCGCGCACCTCGTCTTACCGACGCCGGCCTC
 GCCCAGCATTTACCGCAGCAGTCGCGCTCTTATTATCGCCTGCCCTTGTGCCCTCGGC
 CTGGCAACCCCAACCGCACTTCTGGTCCGAACCGGCCGCGGCGCAACTTGGTCTGTTG
 ATCAAGGGCCCTGAAATCCTCGAATCCACCAAAAAAGTCGACACCATCGTCTCGACAAA
 ACCGGCACCGTCACCACCGGCACCATGTCCGTACCGACGTCACCGCCATCAACTACAGC
 GAAACCGAAATCCTCGAATTCGCTGCAGCCGTGAGTCCGCCTCCGAACACCCCATCGCC
 CAGGCAATCGCCAAGGCCGCCGAACACGAGCAAGTCACCGACTTCCAAAACACCGCAGGT
 CAGGAAGTCACCGGTGTAGTCCGCGGACACGAGGTCCGCGTGGGCAGGCCTTCAAGCAG
 CTTATCGACGCCCTCCTCCACCCCTTCCAACACGCCCAAAAAATCGGCGGAACCCCGTA
 GTCGTACGATTGACGGCGTAGATTCCGGAATAATCACGGTCCGCGACACCGTCAAAGAC
 ACCTCCGCCGAAGCAATCCGCGGACTCAAGGAAGTGGGACTCACCCCAATCCTACTCACC
 GGAGACAATGAAGGCGCAGCTAAATCCGTAGCCGCTGAAGTCGGCATCGACCAAGTCATC

GCCAACGTCCTCCCCACGAAAAAGTCCAAAACGTAGAAGCCCTCCAAGCACAAGGCAAA
 AACGTTGCGATGGTTCGGCGACGGCGTCAACGATGCCGACGCTCTTGCCCAAGCTGACCTC
 GGACTCGCCATGGGAGCCGGCACCGACGTAGCCATCGAAGCCTCCGACATCACCCCTCATG
 AACAAACGACCTCCGATCCGCAGTCGACGCCATCCGACTGTCCCGTAAAAACCTCGGCACC
 ATCAAGGGAAACCTTTTCTGGGCTTTTCGCCTACAATGTTGCACTAATCCAGTAGCGGCG
 ATCGGACTCCTCAACCCAATGCTTGGCGGCATTGCGATGGCCTTCAGTTCAGTTTTCTGTC
 GTCTCCAATTCCTTGCGTCTGCGAGGATTCAAAGCAAGGAGCAAC

>RXA01323-downstream
 TAATGTCCAACAGCGAATGCCAC

>RXA01338-upstream
 ATCCTTGCCCTTGCCAAGGGAAGCCTGTACATGCTGGTCAGGGACATTTTTATGGGTGATA
 ATGGGGTTTATGAATAAAAACTTATACCCCAAATCCCTGG

>RXA01338
 ATGTTATTTCATCCGCTCATTGTGATGGCATCATCACTGTGCGAGCCCTTGTTGCCATCGCA
 ATACATCTCATTTTTATGGCTGGCTCTAGATCTAGATGGCCTTGCTAAAACTGGCCTTTA
 ATAGCCATCGTTATCGTAGGTGGCATTCCGTTGATGTGGGATGTGCTGAAATCAGCCATT
 AAAACTCGCGGTGGCGCGGATACTTTAGCAGCAGTCTCCATCATTACTTCTGTGTGTGTA
 GGGGAGTGGTTGGTTGCCGCGATCATCGTGCTCATGCTCTCTGGTGGTGAAGCGCTAGAA
 GAGGCAGCATCACGGCGAGCCAGTGGCACCTTGACGCACTTGCCCGGCGCGCACCAAGT
 ACAGCTCACCGCCTGTTGGGTGCAACCATTTCTTGATGGAACCGAAGAGATCGCCGTGGAA
 GAGATCACGGTTGGTGATTTAGTGGCGGTGCTCCCGCATGAACCTTGTCCCGTGATGGT
 GAAATCGTGGCAGGCCACGGCACCATGGATGAGTCTTATCTCACGGGTGAGCCCTATGTG
 GTGAGTAAATCTAAAGGTTGCAAGCAATGTCGGGTGCAGTCAATGGTGATACTCCGCTG
 ACGATTGTTGCCACAAAGCTTGCCCATGATTCCAGATACGCCCCAAATTGTTGGTGTACTC
 CATGAAGCAGAAAAACAACCGCCAGAAATGCGCAGGATGGCTGACCGTCTTGCGCGGTGG
 TATACGGTGATTGCACTTGCCCTCGGTGGTCTTGGCTGGATTGTCTCCGGCGACCCAGTG
 AGGTTCTTGGCTGTTGTCTGTCGCCACCCCATGTCCATTGCTCATTGCAGTGCCAGTG
 GCGATCATCGGTGCGATTCTCTTGGCGCTCGTCCGGGCATCATCGTGAAGAACCCTGGA
 ATGCTGGAAAACGCTTCAGGAGTAAAGACAGTGATGTTTCGATAAGACTGGAACGCTCACC
 TATGGCAGGCCAGTGATTACTGATATCCACACTGCTCCCGGAGTTGAGGAAGATACAGTC
 CTAGCTTTGGCTGCTTCAGTAGAGCGCTACTCCAGACACCCGTTGGCTGACGCGATTCTGT
 GAGGGCGCAAAAGCCAGGGAACCTTCATCTGCCTGATGTAGTGGAAGTATCGGAACGTCCA
 GGACAGGGACTAACCGGCACGGTGGGCGAGCACCTGGTTTGAATAACCAATAGGCGCAGC
 AACTAGAAATTGATCCAGACAGCAAGAATACATTCCGGTGACAAGTTCCGGCATGGAA
 TCTGTGGTGCTTGTGATGATAAATATGCAGCACTCATTCGCCTCCGGGATGAACCTCGT
 GCATCTGCCAGTGAGTTCATCGCGCACTTGCCCAAGAAGCACAAAGTGGACAAGCTCATG
 ATTATCTCTGGTGATCGCGCATCTGAGGTTCTGTTACCTTGCGGACAAGGTTGGCATTGAT
 GAGGTACACGCAGAGGCTCACCAGGAAGACAAGCTGAACATTGTTAATCGGCATAATGAG
 CACGGCGCCACCATGTTCTTAGGTGATGGAATCAACGATGCGCCAGCCATGGCCGTTGCC
 ACCGTTGGTGTGCGGATGGGAGCAGACTCCGATGTACGTCCGAAGCAGCAGATGCTGTG
 ATTTTGGATTCTTCCCTGGAACGTCTCGACGATCTGCTCCACATCAGTGCACGGATGCGT
 CGAATAGCGTTGCAATCTGCGGGCGGTGGCATGGCGTTGAGTGTATAGGAATGATCCTC
 GCGGTATTTGGATTCTTGACGCCACTGATGGGTGCGATCTTCCAAGAGGTGATTGACGTG
 CTGGCTATCTCAATTCGCTCGGGTTCGCACTGCCACGCGGAGCGATTAGTGATTTTGAT
 ACGCAAGAAAAAGTTTCT

>RXA01338-downstream
 TAGCAGGGTAACCTAAATGTCTG

>RXA01395-upstream
 CTCAAAAGCACTGATAAAAGCAGTCAACCCACCTCGGGTTGGCTGCTTTTTTGCATCCAG
 ATGCACAAAGCCGTGGCACAACGAGACAACTGAGCACA

>RXA01395
 ATGGCTGTCTATGGCATATCAACCAGCAGACAATCGCTATGACGACATGATCTACCGCAGG
 GTGGGAAATTCTGGGCTGAAGCTTCCGGCAATTTGCTTGGGCTGTGGCACAACCTTCGGT
 GATGACAAGCCGCTTTCAACGCAGCGCAGCATTATTCACCGCGCGTTTGATAGGGGAGTC
 ACTCACTTCGATTTGGCTAATAACTATGGACCTCCAGCAGGTTCCGCAGAGACCAACTTT

GGCAGGATTTTGCCTGAGGATCTCAAAAGCCACCGCGATGAGTTGATCATTTCTTCCAAG
GCGGGTTGGGATATGTGGCCTGGACCTTATGGTTTTGGTGGTTCCCGAAAAGTATCTAGTG
AGTTCCCTTGATCAGTCCCTGACTCGCCTCGGCTTGGATTACGTGGATATTTCTATCAT
CACCGCCCGGATCCAGATACTCCTTTGGAAGAAACCATGTACGCATTGCGTGACATTGTT
GCGTCTGGAAAGGCTCTTTACGTGGGTATTTCTTCTACGGTCCAGAGCTCACAGCGGAG
GCGGCTGAGTTCATGGCGGAGGAGGGCTGCCCCGCTTCTGATTTCATCAGCCAAGCTATTCC
ATCATTAAATCGTTGGGTGGAGGAACCGGGCGATGACGGTGAGAACTTGTGTCAGTCAGCT
GCCAACAAATGGTCTTGGCGTCATTGCTTTCTCACCCTTGGCGAGGGCTGCTCACGGAC
AAATATCTCGATGGAATTCCAGAGGGTTCCCGCGCCAGCCAGGGTAAGTCCCTKTSTKAC
GGSWTGTTGAACGTGAACAATATTGATWTGGTCCCMARSYTNWKRSAWTTTCCMARRAM
ACCGGGCAGTCTTTNNCCNAAAGGNCTTTTGTGGGTGTTGCCCAACCAAGGAAAAGTA
CGGCGCCGGATTACCGTGACCACTGTCATTGATTGGTGCTTCGTGAGTTCAGCAGCTGGAC
AACAGCCTTGATTCACTCAACAACCTGGAGTTTTCTGACCCGAGTTGGAGGCGATCGAT
GAGATTTCCACGACGCCGGCATCAACATTTGGGCGAAGGCCACCGATTCCAAAACCCGC
GAAAAC

>RXA01395-downstream
TAACCCATCAACATCAGTTTGAT

>RXA01411
TTCATTGCGCAGGTAATGCTTGGAAATCGGCGCGGTTACCGCTAACTGCGTTACCTCAGTA
ATGATGGCCGAGGTCTTCCAAGAGGTACCCGCGGTACTTCCGCCGGCATTACCTACAAC
GTCATTACGCAATCTTCGGCGGCTCGGCTCCATTTATCTCCACCGCATTGGTCTCCTGG
ACCGGCAGCCCGCTGGCCCCCTGCGGTATACATGATCATCATTGCGCTCTTCGCCTTACC
GCGTCCCGCTTCATTCTGAAACCTCCCGAGTTTTTGTACCCGCAACCCCGGCCATTAAAG
GCACCAAAGGTGCTGGTCAACCCGGGT

>RXA01411-downstream
TAAACCACGCTTTTCGACGAAAA

>RXA01454-upstream
GGCCAGGACTTTGGCGTTTCGGATCAGCAGTTCGGCTTGGATTATGGATTCTACGCGTTT
GATCTTCCGATGCTTCGCCTCATCGCTTGACTCACTGTCTG

>RXA01454
ATGATGTTGATCGTTGCTTTCTGATCGCACTCGTTGGCCATTACCTCATGGGTGGCATT
CGCGCTGGAAACCAGATGACGGGGCCAGAAGTCCTTTGTATCCCGTGGTGCGCGCACTCAG
CTTGCGGTAAGTCTGTTGATGCTTGTAAAGGTGCTGGCTACTGGCTGGATCGC
TATGACCTGCTGACTAAGGAAAACCAACCTTCACAGGTGCAAGCTACACCGACATCAAT
GCACAGCTGCCAGCGAAGATCATCCTG

>RXA01455-upstream
AGAGTGGGGGAGAAACGCATAATCACGTACATATAAGGATATTGTCTTGTGCTGACTGGTCT
CACACCTCCTCCCAACCGATCAAGCGACCTCCCAAGGCG

>RXA01455
GTGACATGGATCTTCGCCATTATCGCGTTGGTCACTTCTCATCGCCCCAATGAGTGTTGGC
TTCTATACCGACTGGCTTTGGTTCCGGTGAAGTCGATTTCCGAGGCGTTTTTCAGCAAGGTT
ATTGTCACTCGCATTGTTCTCTTTGTGATCTTTGCGCTAATTGCTGGGTTTGTACATGG
CTTGCTGGTTATTTTGTGACAAAACCTCGACCTGATGAGATGTCGGCGTTTGATACCCAG
TCGCCTGTGTATCAGTACCGTCAGATGATCGAAAACAGCCTTCGTGCGGTTATGGTGATC
ATTCCAATTTTCGTGCGGTTGCTGGCTGGCCTAATTGGTCAGCGTTTCGTGGCGCACCGTT
CAAAATGTGGCTGAATGGCCAGGACTTTGGCGTTTCGGATCAGCAGTTCGGCTTGGATTAT
GGATTCTACGCGTTTGATCTTCCGATGCTTCGCCTCATCGCT

>RXA01455-downstream
TGACTCACTGTGATGATGTTGA

>RXA01625-upstream
GGGAGCGAAGTTCCCTGGGTAAATTAACCACTGCAGTATACCCTAGTGGGGTATATTG
TCTGCTGTAGAAAGATACCCGACAGAAAGGGCCAATAAT

>RXA01625
ATGGCTATCAAGAACTACACCGTCGAAGGCATGACTTGTGGACACTGCGTCTCCTCCGTA
AAGGAAGAGGTTCGGAGAGGTTGCTGGCGTCACCGCTGTGGACGTCACCCTAGAAACCGGT
GCCGTGCAGGTTACCGGCGAAGACTTCACCGACGAGGCTGTCAAGGCTGCTGTCTGAG
GCTGGCTACAAGGTTGTTGCA

>RXA01625-downstream
TAAACCCCTGAAAAGTTTAAAGC

>RXA01756-upstream
GCTTCAAACAGGATTTAATCTAAATCTTAAACCTCGTATTTTCCCTGATAGGCTCAGAT
GCGCCTGAAATCGGGCTTGTTGAGGGGAGAGGTGTGTGAC

>RXA01756
ATGAAAGAGTTGGAAGTGGGCGAGGCGAGGGACGTCGCTGCAACGTTGGAAGCGATGCCG
ATCCAGGAGGTTATTGATCAGGTTGAGCGAACTTCTATAACTAAAGGTGCGGTACTGCTG
CGTCTGCTCAGTAAAGATCGATCGTTGTTGGTCTTCGATGCTCTTGGTCCGCGACTCCAG
GCTGATCTCATTGGTGCTTTTCAGGATGCGGAAGTGCTGGATTATTTGCTGACCTTGAC
CCTGATGACCGGTTTCACTGCTTGATGAGCTGCCGGCGTCGATCGCTGACGAGTTGCTT
CGCAGTCTCGATCCGAGGAAAAGCAGGTCACGGAGCTGGTCTTGGGTACGCAAAGGGG
TCGGTTGGACGTTGGATGTGCCCCAGGTTTTATTGCTTTTCGACGACATGTCCGTCGCC
GAAGTCTTAGATTTTGTGCGCAATCATGCTGCTGAGGCTGAGACGATTTATGCCTTACCT
ATTGTGAACCGTGCTCGCCAAGTGATGGGCGTGGTGTCTGTTGCGAAAGCTGTTTCATCGCA
GATCCCACTCTAAAAGTCTCGGAAATCATGGTGCGTCCTGTTTCGGTGTTGGCGTCCGCG
GATATTGAAGAAACCGCCCGCTGGTTTCTACAGTTGGACCTCGTTGCGATGCCCGTTGTG
GATGAATCGAATGCTCTTAGGAGTGCTGACCTTCGATGATGCGCAAGACATCGTGGAG
CAAGCCGACTCTGAGGACTCCGCTCGCAGTGGTGGTTCGGAACCTCTCCAGCAGCCGAT
CTATCCACGCCGATTTCGGAACCTGGTGAAGTCCCGCATCGTATGGCTTCTGGTTTTGGCA
GTGTCAGCAATTTGACGGTTCAAGTTCTTGATATTTTGAAGCCACCTTGGTTGAAGCC
GTGGTACTGGCATTTGTTTCTTCTGCTCACTGGTACTGGCGGAAACACCGGAAACCAA
GCTGCAACAACCGTGACCCGTCGCTCGCAATTGGGTGACGTCGGAATTCAGATGCTCTTC
CGCGTCTTGGGCGAGAGAAATCCGAGTCCGCTCATGCTCGGGGCATTGTTGGGTGCCGTT
GGATTTGTGATCGCATCGCTTGTTTACGGCATGCCCGTAGGCACTGTCATCGGTCTGACA
TTGTTGGCGGTGTGCACGATGGCCGCATCAGTTGGCGGAGTAATGCCAATTATTGCCAAG
GCGATCGGAGCGGACCCAGCGGTGTTCTCTAATCCTTTTATTTCAACCTTCTGTGATGCA
ACAGGTTTGATCATCTACTTTGCAATTGCCAAGTTGGTGCTCGGAATC

>RXA01756-downstream
TAAAAGATTTTTCGTTTTCGACG

>RXA01808
ATGCGCGGCGGTGCACCAGCGCGAACCTCAAAGCCTGGATTCCGCCTTGAAGCCGCGGAA
GCTTTGATCGCAGAAGTGCCAGCGCCACGCGACAAAGTCGAGCTCATGGCATTTCCTCAAG
TCCAGGCAAGGCCGCGTTGTCAATTGAACCTGAAGACGCCACAGTAGCCACCCCTGATGAT
CGCATCCTGGTAGAAGACCTCACCTGGCGTTTGGCTCCAGGAGAGCGCATCGGTCTTGTC
GGCGTCAACGGCTCCGGCAAAACCACCTGCTGCGCACCTTGGCGGCGAGCAGCCACTT
CAGGCAGGCAAAACGCATCGAAGGCCAAACCGTCAAACCTGGGATGGCTCCGCCAGGAATC
GATGACCTAGACCTCAGCCGCCGACTCATCGACTGCGTTGAAGATGTGCTTCTACGTG
ATGATGGGCGACAAGCAGGTCTCCGCTTCCCAATTGGCAGAACGCCTCGGATTCTCACCC
AAGAGGCAACGCACCCAGTTGGTGACCTGTCCGGTGGTGAACGCCGCCGACTCCAACCTC
ACCCGCGTGCTCATGGCCGAACCAAACGTGCTGCTCCTCGACGAGCCACCAACGACCTG
GACATTGACACCCCTCCAAGAGCTGGAATCCCTTCTCGACGGATGGCCAGGCACCATGGTG
GTTATCTCCACGACCGTTACCTCATCGAACGCGTCACCGACTCCACCTGGGCACTCTTC
GGCGATGGCAAGCTCACCAACCTGCCAGGCGGAATTGAAGAGTACCTGCAGCGACGAGCA
GCGATGGCCGCGGCGAAGACAGTGGAGTGCTGAACTTGGGTGCGGCCACGAGGCTGGA
ACCTTTTCTGCTGCAACAGAGCAGGCTGCCACTTCTGTGGAAAGTTCCGGAATTTCTTCC
CAAGAACGCCACCGCATCACCAAGGAAATGAACGCCCTGGAGCGCAAAATGGGCAAGCTT
GACCAGCAAATGGACAAGCTTAATCAGCAGCTCGCTGATGCAGCGGAGGCCATGGACACC
ATAAAGCTCACCGAGCTGGACACCAAGCTCCGCGCAGTGCAGGAAGAACACGGCGAGCTG
GAAATGCAGTGGCTGGAACCTCGGCGAGGAAATCGAGGGC

>RXA01808-downstream
TAGTTCATGCCGTCGGCAGGCGA

>RXA01822
ATGGCCAGACAAAATAGCAATACCGGCGGGTTGCGTCTGGTGTGGTTGGTATCGGAACA
GGTGCAATTTTTGGGTGCTGCTCGTGATTTCTTCATGGTGC GCGCAGATATTACGGGTGCT
TCGACGGTACAGCTGTGGTCTGCCGGTTCGTTGAGCGGGCGCGACTGGAATCATGCCCTG
TTGGTGTGATTTCGTGTGCAGTGATTGTGCCAGCACTGTGCATTATTGTCCGCCGTTTA
CGCCTGATGGAAATGGGTGATGATGCAGCTGGGGCACTTGGAATTTTCAGTGAGAGAGAACA
CGGTTGATAGCCATTTTGTGGCTGTGCTGCTGGTGGGGATCGCCACCGCAGCTGCAGGT
CCCATCGCTTTTATTGCACTGGCAGCACCTCAGATTGCCCCGGGCTCTGGCCCCGGGAGGAT
GGAGTGCTGGTGGCTGCGTCGATAAGCATTGGCTCTGGGCTGTTAGTTGCGGCGGATTGC
CTAGAGCAACACGTTGATACCTGAGCTGCACACGCCCGTTGGCCTGGTGACCAGTTTGCTG
GGCGGGGTGTATTTGATGTGGCTTTTGAGCCGAAAGGAGGCA

>RXA01822-downstream
TAAATGCTGCAAGCGCATGATCT

>RXA01890-upstream
GCTGAGGTTGAGACCAAGCTGAACACCATCTACACCCGCGACATCGAACCCTTATTTAA
TCCGAGCACTTCAGCTACACCTATTTAAGGAGGCTGTGAC

>RXA01890
ATGGCGTCAATCGTCTTTGAAAACGTACACGCAAATACTCTCCGGGCGCACGCCCCGGCC
GTCGACAAGCTTAATTTGAAAATCGCCGACGGCGAGTTCTAGTTCTCGTTGGACCCCTCA
GGCTGTGGAAAGTCCACTTCTTTGCGCATGCTGGCTGGTCTTGAGCCTATCGACGAGGGGA
CGTCTACTCATTTGATGGTAAAGACGCCACGGAACCTGCGTCCGCAGGATCGTGACATCGCT
ATGGTCTTCCAGAGCTACGCGCTGTACCCGAATATGACTGTTCCGGGACAACATGGGCTTT
GCGCTGAAGAATCAGAAGGTGGCTAAGGCTGAGATCGAAAAGCGTGTGCTGAAGCCTCA
CGCATTTCTGCAGCTGGATCCGTATCTTGATCGTAAGCCTGCAGCTTTGTCTGGTGGTCAG
CGCCAGCGCGTGGCCATGGGCCGTGCAATTGTGCGTGAGCCATCGGTGTTCTGCATGGAT
GAGCCACTGTCCAACCTAGATGCGAAGCTGCGTGTGTCTACGCGTGCGGAGATCTCTGGT
TTGCAGCGTGCATGGGCGTGACCACGGTGTATGTGACTCAGCATCAGGTGAGGCCATG
ACCATGGGTGATCGCGTGTGCTTTTGTCTCGGTGTGCTGCAGCAAGTAGACACCCCCG
CAGAACCTGTACGACTACCCAGCAAATGCGTTTCGTGCCAGCTTCATTGGTTCCCTTCCA

>RXA01890-downstream
TGAACCTTGATTGAGGGCACCATC

>RXA01900-upstream
AAAGGTGACACGCCCTTACATTCTTGTGGTCTGACCATGAGGTTGGGCCAATCGGTTTCAG
CCCGTTTACTCCCGCGTCCGTTTCAGAGAAGAGGTCACC

>RXA01900
ATGACAACCGCAGTAGATCAAACTCACCGCCCAAGCAGCAACTCAACAAGCGCGTCCTG
CTGGGCAGCTTGAGTGGCAGCGTTATCGAATGGTTTCGACTTCCTGGTTTACGGAACCGTC
GCCGCGCTGGTCTTCAACAAGATGTACTTCCCCAGCGGCAACGAGTTCTCTCCACAATC
CTGGCGTACGCATCCTTCTCCCTGACCTTCTTCTTCCGCCCCATTGGTGGCGTCATCTTC
GCCCACATCGGCGACCGCATTTGGGCGTAAGAAGACCCTGTTTATCACCTTGATGCTCATG
GGTGGCGGCACCGTCGCCATTGGTTTGTGCTGCCCCGACTACAACGCCATCGGCATTTGGGCA
CCAATCCTTCTGATGTTCTTCCGCATTTTGCAGGGCATCGGAATTGGCGGCGAATGGGGT
GGCGCACTGCTCCTGGCATAACGAATACGCTCCAAAGAAGCAGCGTGGGCTCTACGGCGCA
GTTTCTCAAATGGGCATTTCCCTGGGCATGCTGCTTGACGCTGGCGTGATCTCTTGCTC
ACCCTCATGCCGGAAGATCAGTTTCTCACCTGGGGCTGGCGCATCCCATTGCTCGGATCC
ATCCTCCTAGTGTTTCATCGGCCTGTTTCATCCGAAACGGCCTTGATGAAACCCCCGAGTTC
AAGCGTATCCGCGATTCCGGCCAGCAGGTAAAGATGCCTCTGAAGGAAGTTCTGACCAAG
TACTGGCCAGCCGTTCTGGTCTCCATCGGCGCAAAAGCTGCCGAGACCGGCCCTTCTAC
ATCTTCCGCACTACATCGTTGCTTACGCAACCAACTTCTGAACATCCGCGACAACATT
GTCCTTCTGGCAGTTGCTTGCGCCGCCCTCGTTGCCACCATCTGGATGCCACTGTTCCGA
TCCTTCTCCGACCGCGTCAACCGTGCAAGTGTCTACAGGATCTGTGCATCCGCAACCATC

GTGCTGATTGTCCCTTACTACTTGGTCCTCAACACCGGCGAAATTTGGGCACTGTTTATC
ACTACCGTGATTGGCTTCGGCATCCTCTGGGGTAGCGTCAACGCAATCCTCGGAACCGTC
ATCGCAGAAAACCTTCGCACCTGAGGTCCGCTACACCGGCGCTACCCTGGGTTACCAAGTC
GGAGCAGCACTCTTCGGCGGTACCGCACCCATTATCGCAGCATGGCTGTTTCAAATCTCC
GGCGGACAATGGTGGCCAATCGCCGTCTACGTGCTGCATGTTGCCTTCTCTGTGATC
GCCTCGTTCTTCATCCAACGCGTCGCGCACCAAGAGAAC

>RXA01900-downstream
TAAATCTAAGTAAAACCCCTCC

>RXA01939
TCTACAAGCGGCACCGATCTTACGTCTTGAGCCACAAGGAAATCTTCCAAATGCGACGC
AAACTGCAGGTGGTGTTCAGAACCCCTACGGCTCGCTTGATCCGATGTACTCCATCTAC
CGGTGTATTGAGGAACCGCTGACCATCCACAAGGTTGGTGGAGACCGCAAGGCACGCGAA
GCTCGCGTCGTTGAACCTTCTCGATATGGTGTCCATGCCAGGTCCACCATGCGCCGCTAC
CCCAACGAGCTTTCCGGTGGCCAACGTGAGCGCATCGCCATCGCCCGTGCATTGGCACTG
AATCCAGAAGTGATCGTGTGGATGAAGCGGTTTCCGCTTTGGACGTGTTGGTTCAGAAC
CAGATCCTCACCTGCTTGCAGAACTTCAGCAGGAACTGAAGCTCACCTATTTGTTTCATC
ACCCACGACTTGGCCGTTGTTTCGACAAACCGCCGACGATGTTGTGGTGATGCAAAAGGGA
CGAATCGTTGAAAAGGGTCTGACCGACGACATCTTCAACGATCCTCAGCAGCACTACACC
CGCGATTTGATCAATGCGGTACCTGGTCTGGGAATCGAGTTGGGTACTGGAGAAAACCTG
GTT

>RXA01939-downstream
TAACCCGCACAGCCTCACTAAAC

>RXA01972-upstream
ACGCGTTGCTGGATATCACCTGGCCGTGATGACAACGCCGAATGCATCGACGCCGGAT
GCGCCGTACCTGGGTGTGTCACTGGACAGGAGAGTGCCTA

>RXA01972
GTGGCAACCGGTCTACTGTGCGCGATTGGTCTGTTTATCGCCACCAATATCGACGACATC
ATCGTGCTCTCGCTGTTTTTGGCCGCGGGGCGGGGCAAAAAGGGACCACGCTTCGGATT
CTGGCTGGTCAGTACCTCGGCTTCATGGGCATCCTCGCGGCCGAGTCCCTGGTCACGCTG
GGGGCAGGAGCATTCCTACCTGCTGAGGCGATCCCGTACTTCGGACTAATTCCTCCCTGGCC
CTGGGACTATGGGCGGCCTGGCAGGCCTGGCGAAGCGATGATGACGACGATGATGATGCG
GAGATCGCCCGGAAAAAGGTGGGTGTGCTGACCGTCGCCGGTGTGACGTTTGCCAAACGCT
GGCGACAATATCGGCGTCTACGTCCCGGTCTTCCTCAACGTGGACACTGCCGCCGTCTATC
ATCTACTGCATCGTTTTCTCTGCTCCTGGTGGCAGGCCTGGTCCTGCTGGCAAAGTTCGTG
GCCACCCGCCGCCCATCGCAGAAGTCTTGAGCGCTGGGAGCACGTGCTGTTCCCGATC
GTCCTGATCGGCCTGGGCATCTTCATCCTCGTCAGCGGCGGCGCCTTCGGCCTC

>RXA01972-downstream
TAATAAGCCCATCCCGAGCGCCC

>RXA01986-upstream
GCCACGATTAAAGACATTGGTGATGTGAATCACTGCCTACTACATCGTGTTCGTGACCC
TGCACCTCCAAGTAAGGGCAGGACAACTTAGGAGACAAG

>RXA01986
ATGGCTAGTACCTTCATTACAGCCGACAGCCCTGAAAAAAGTAAGAAGCTGCCCCCACTC
ACAGAAGGTCCGTATAGAAAGCGGCTATTCTACGTTGCACTAGTTGCGACGTTTGGTGGG
CTGCTCTTCGGATATGACACCGGAGTAATCAACGGTGCACTCAACCCAATGACACGTGAG
CTCGGACTAACCGCGTTCACCGAGGGTGTGTAACTTCTTCCCTGCTGTTTGGTGCAGCA
GCTGGTGCGATGTTTTTTCGGTTCGATTTCCGACAACCTGGGGTCGCCGAAAAACAATCATC
TCACTTGCACTAGCTTTCTTTGTCGGCACCATGATCTGCGTGTGTGCTCCATCTTTTGCA
GTAATGGTTGTGCGACGTGTGCTTCTTGGACTCGCAGTTGGTGGCGCTTCCACTGTTGTC
CCTGTCTACCTGGCTGAACCTGCTCCTTTTGAATCCGTGGCTCACGCTGGCGGTAAT
GAGTTGATGATTGTTGTTGGTCAGCTCGCAGCTTTTGTCAATCAATGCGATTATTGGAAAT
GTTTTTGGACACCAGATGGTGTGTGGCGCTACATGCTGGCAATTGCCGCAATCCCAGCA
ATTGCCCTCTTCTTTGGA

>RXA01995-upstream

CCGACGCAAAGGCATGCGCCTGCGTGTCTCGAGTAGTCTCCTCCCCTTCCTCGTCCCCAA
CCTCGACCATTACGGTCGCCCTCTCCTAAAGGAGCCTGGC

>RXA01995

ATGGATATCCGCCAAACAATTAACGACACAGCAATGTGAGATATCAGTGGTTCATTGTA
TTTATCGCAGTGCTGCTCAACGCACTGGACGGCTTTGATGTCCTCGCCATGTCTTTTACT
GCGAATGCAGTGACCGAAGAATTTGGACTGAGTGGCAGCCAGCTTGGTGTGCTGCTGAGT
TCCGCGCTGTTCCGGCATGACCGCTGGATCTTTGCTGTTCCGGTCCGATCGGTGACCGTTTC
GGCCGTAAGAATGCCCTGATGATCGCGCTGCTGTTCAACGTGGTGGGATTGGTATTGTCC
GCCACCGCGCAGTCCGCGAGGCCAGTTGGGCGTGTGGCGTTTGATCACTGGTATCGGCATC
GGCGGAATCCTCGCCTGCATCACAGTGGTGTGATCAGTGAGTTCTCCAACAACAAAAACCGC
GGCATGGCCATGTCCATCTACGCTGCTGGTTACGGCATCGGCGCGTCTTGGGCGGTTTC
GGCGCAGCGCAGCTCATCCCAACATTTGGATGGCGCTCCGTGTTTCGACGCCGGTGGCATC
GCAACTGGTATCGCCACCATCGCTACTTTCTTCTTCTGCCAGAATCCGTTGATTGGCTG
AGCACTCGCCGCCCTGCGGGCGCTCGCGACAAGATCAATTACATTGCGCGCCGC

>RXA02033-upstream

TGATCTGCTGTATCAGGTGGTTGATCCAAGAGTCGGTGCTGTTGGGGTTGCTAGCACTAA
GGTTCAGGGAGCGTGGCTTAAGTGACAACGATCAAAAAC

>RXA02033

ATGCCCCCTTTCAGGGAAAATCGGCGGCTTCATCGTTGCCGTTGTATTTGTTCTTGCTGCG
CTGTCTTTTCATTTGGACTCCGTTTGATCCAGTTCAAGCTTTCCACAGGAGCGCCTTGAG
GGAAGTTCTTTGAGGCACCTGTTGGGAACGGATCGTTATGGTCGCGATGTTTTATCCAG
ATCATGGTTGGTTCCCGCGTCACGTTGTTGGTGGGCATCATTGCGGTGGCGATCGCAGCA
TTAATCGGCACGCCACTGGGTATTGCTGCGGGAATGCGCCGTGGCATGGTGGAAACCTTT
GTCATGCGTGGTGCCGATTTAATGTTGGCGTTCCAGCACTGTTGTTGGCGATTATTTCC
GGCGCCGTTTTTCGGCGCCTCCACGTGGTCCGCGATGGTTCGCGATCGGCATCGCAGGCATC
CCTAGTTTTGCCCGGTGGCTCGTGACGGCACATTGCAGGTGACCACTCAGGATTTTCATC
GCAGCTGCTCGGCTATCAAAAGTAAGTTCCGCGCGGATCGCGCTTCGCCATATTTGCC
AACATCACCAGCATGTTGATCGTTTCAGGCATCAGTAGCTTTTGCCCTGGCGATCCTGGCG
GAAGCCGCATTGAGTTTCTCGGTTTGGGCACCACTCCCCCGGATCCAGCTGGGGTTCGC
ATGTTGCAAACCGCTCAAGCATCCATCGGCGTCACCCCATGTTGGCGGTGTGGCCCGGT
GCTGCGATCGCTTTGACGGTCTTGGTTTTAATCTTTTCGGTGATGGTTTACGCGATGCC
ATCGATCCA

>RXA02033-downstream

TAGTATTATAT

>RXA02034-upstream

TCGTGGTGATGTCACCAGAGATCACCGGCATTGATCCCAACGTGGTGTCGGGGCGTTGG
AATTGTCGTTGATTGGTCGAAAGAATCCGGGGTAGCGCA

>RXA02034

GTGAGTAAACAATCGCTTGGACTGTGCTGCGGTACACCCTGACTTTTGTGATCGCCAGC
ATCATCATTTTGTGCTGATTGAGTCATCCCCGGTGACCCGCGCTGTTGCCCTGGGA
ATTACCGCGACACCAGAAGCAATCGCTGCGTTGCAATCACAATTAGGTAAGTACTGATCAACCG
CTTTTCCAACAGTACTTTTCCCTGGATAGGTGGAATGCTCACTGGCGATTTTCGGCACCTCG
CTGAGCTCTGGCCAAGACCTTTCCCCCATCATTTTGGACCGCTTACAAGTGAGCCTCATT
TTGGTGGGATGCTCCATTGTGTTGTCGTTGCTCATTGCCATTCCACTTGGTGTGCTTTTCG
GCCCCGCGCGGTGGCGTGATCATTTCCGGCATCAGCCAGATTGGCATTGCGATCCCTAGT
TTCCTCGCCGGTATTTTGTGTTGCTGCTGCTTCGCCGTTGGTTTGGGGTGGCTGCCCGCC
AATGGCTGGATTCCGCCGTCGGAAAACCTTTGGAGGTTTCTTAGCCAGGCTGATCCTCCCG
GTTCTGGCTCTTACTGCTGTTCAAGCAGCAATTTTGACCCGCTATGTCGCTCTGCAGTA
ATGGATGTAATGGGGCAAGATTTTCATGCGCACCAGGTCGAAAGGTATGAGCTTCAAC
CGCGCGTTGATCATCCACGGTCTTCGGAATGCTGCTCTTCTGTCCTTACCGTCACTGGT
TTGCAGCTAACAACCTTGGTTATCGGCGCCGTGGTGATTGAACAAGTCTTTGTATCCCC
GGAATCGGTTGATGCTGCTGGAGTCCGTGTCCAACCGTGATCTCATCGCTGTGCAATCT

ATTGTCATGCTGCTGGTGGCGTTACGTTGCTGGTTAATTTGGTGGTTGATCTGCTGTAT
CAGGTGGTTGATCCAAGAGTCGGTGCTGTTGGGGTTGCTAGACTAAGGTTCCAGGGAGC
GTGGCT

>RXA02034-downstream
TAAGTGACAACGATCAAAAACAT

>RXA02035-upstream
GGATTTTCCATTGGCGGAGGTTTCATGCGGCGGGTATCCATTGCCTTCCATTTTAGTTTTTC
CATTTAGTTTCCCGGATCACACCGACTAATCTCAGAAGCC

>RXA02035
ATGAAGATCACGCGCGGACTCCTGCCATCATTGCTGTTGGCAAGCACAAATCGTGGTGTCTG
TCATGCTCTGCTGGATCGACTGCGTATCAGCAGCCCCCTGCTGTTGATCAATCATCCATT
GTCATTGCTACCACGGCTGCTGCGGCGTCACCTTGATTTCACCAATGCTGCGGGCGCTGCT
ATTCGCGAGGCGATGATGTCCAATATTTACGAGGGGCTTGTGCGCATCGATGCGGAGGGT
GAGATTACGCGCTGCTTGCCACGTCGTGGGATATTTACGACGATCGCACCGAGTACATT
TTCCATTTGCGGGAGGGTGTGCTGTTTTCCAACGGCGATCCCTTCAATGCTGATTCTGCG
AAGTTTTCCATTGATCGGGTAAAACTGACTGGACCAATGGTTTAAAAAGTGGCATGGAT
GTGGTGGAGTCCACCGAGGTGATTGACGATCACACGCTGAAAGTTTCGCTGGTCAGGCCG
TCCAACCAATGGTTGTGGAGCATGGGTACCGCGATCGGTGCCATGATGACGGAGGGGGGC
GTCGATAAGCTGGCAACTGATCCCGTTGGCACCGGCCCCGTACACGGTGACGCACTGGGCG
CCGGGCCGCGCAATTGGGTTTCGGCGCGCGGGCCGATTATTGGGGGCAGAAGCCGCTTAAC
GACGCCGCAACCATCCGCTACTTCAGCGATGCGACGGCCTCGACCAATGCGCTGCAAAGC
GGTGACGTGGACGTGATTGGGCGATGCAAGCGCCGAACAGCTGGCTACGCTGCAGGAA
TACACCGTGGAAGTGGGCACAACCAATGGTGAGATGTTGCTGTGATGAATAATCAGCGT
GCACCTTTTGATGATGTGCGTGTGCGCCAGGCGGTGATGTTTTCGATTGATCGCCAAGCC
GTCATTGATACCGCGTTGGAAGGTTACGGCACCGACACTGGTGGCGTGCCTGTTCCGCCG
ACTGATCCGTGGTACGAGAAATCCACGATGTACCCCTACGATCCGGACCGCGCACGGGCA
TTGTTAGAGGAGGCCGGCGCCGAGGGAACGCGGATCACCATGTCCATTCCCTTCGTTGCCG
TACGCTCAGGCAGCCTCTGAAATCCTGTACTCGCACTGCGAGATGTTGGTTTTGATCCT
GTGATTGAATCAACCGAGTTCCGAGCCGTCTGGTTGGCAGAGTTCATGGGGCAAAAAGAC
TACGACATGTCACCTAATCGCGCATGTGGAACCCGCGACATCCCCACGCTGTTTAGCCCC
AACTACTATTTGGGCTTTGACGACACCGAAACCCAAGCCCTCCTCGCAGAGGCAGACAGT
TCAGCAAACGAAGTGAATGATGCAACAAGCTGTGATCGAATCATGGAACAAGCCGTC
GCCGACAACCTCATGAACGTGGCCAACATCGTGGTGATGTCACCAGAGATCACCGGCATT
GATCCCAACGTGGTGTCCGGGCGTTGGAATTGTCGTTGATTGGTCGGAAGAATCCGGG
GTAGCGCAG

>RXA02035-downstream
TGAGTAAACAAATCGCTTGGACT

>RXA02062-upstream
TTGTCTAAACATCGTTTTGGGGTCCGAATGATAGCCCCCTTTAATGCCCCCATTTTCGGTA
TCGCTGCGCAACTGTTTTTAGATGGCTAATCTTTGAAATT

>RXA02062
ATGAGAGTCGGAATGATGACAAGAGAGTATCCACCAGAGGTTTACGGCGGCGCTGGCGTG
CAGGTCACCGAATTGACCCGATTTCATGCGTGAGATCGCTGAAGTTGATGTTCACTGCAATG
GGTGACCTCGCGATATGGAGGGAGTTTTCTGTCACGGCGTCGATCCTGCCTTGGAAAAGC
GCGAACCCTGCGATTAAAGACACTGTCCACCGGTTTACGCATGGCAGAAGCTGCAAAACAAC
GTGGATGTGCTGCACTCACACACTTGGTATGCAGGTCTTGGCGGCCACCTTGACGCTCGT
CTCCACGGCATTCCTCACGTGGCTACCGCGCACTCTTTGGAGCCAGATCGCCCATGGAAG
CGTGAGCAGCTTGGCGGTGGATACGACGTGTCCTCCTGGTCTGAAAAAATGCCATGGAA
TACGCTGACGCGGTTCATCGCTGTGTCGGCTCGCATGAAAGATTCCATCCTCGCTGCGTAC
CCTCGCATCGAGCCGGACAACGTGCGTGTTGTCTCAACGGCATCGACACTGAGTTGTGG
CAGCCTCGCCGACTTTCGATGACGCGGAAGATTCCGTACTCCGCTCCCTAGGCGTTGAC
CCACGCGGGCCCATCGTCGATTTGTGCGCCGCATCACCCGCCAAAAAGGCGTCGAGCAC
CTCATCAAGGCAGCAGCGCTTTTCGACGAGTCCGTGCAGCTTGTGCTCTGTGCCGGCGCG
CCAGACACCCCCGAAATCGCAGCTCGCACCACCGCCCTGGTGGAAGAACTCCAGGCAAAAG
CGCGAAGGCATTTTCTGGGTTTCAGGACATGCTGGGCAAGGACAAAATCCAAGAGATTCTC

ACCGCTGCTGACACCTTCGTGTGCCCATCCATTTACGAGCCACTGGGCATCGTGAACCTTG
GAAGCAATGGCCTGCAACACCGCAGTTGTGCGATCCGACGTTGGAGGCATCCCTGAGGTT
GTTGTGACGGCACCACCGCGCCCTCGTTCACTACGACGAAAATGATGTCGAAACCTTC
GAGCGGATATCGCCGAAGCGGTGAATAAAATGGTCGCTGATCGAGAGACCGCAGCCAAA
TTTGGTCTCGCAGGGCGCGAACGTGCTATCAATGATTTCTCCTGGGCAACGATTGCTCAG
CAGACCATTGATGTGTACAAATCCTTGATG

>RXA02062-downstream
TAAAACCGAAAGCCGGGGAACCT

>RXA02068
ATTTTGTCCCCATGTTGCGTATCGCTGCCATTGAACCGAAAGACATTACTTTGGTTACC
GGTTCTGTATCACTTCGAACCTTTTCGCGTGCGCACCGGTGAATTGCAGGTCATGGGCGAT
ATTGTGGGTGCAAAAGTACATACCGATGATCCAGAGCTGCAACAATCCACGGTCGCGCG
GTAGAAATCGCCGATGTGGAGCTGGAGTTATCGCGCACTCGCGATTGGATCATCACGCGC
GTGGCGGTGCTGGGTGAGCGCCCTAAATTTGGCCGGCGCCAGTGCTGCACACAGTGCCG
TGGAGTCATATCCACGGCATCACCGCAGGTGGTGTGCGCGAGTCCAATCACACCGCCGAA
CTCATCGCAGGGTTTGAGGATATGAGGCCTGCGGACGTGCGAAAGCAGCTTTATCAGCTG
CCTACGGCTCAGCGTACCGAAGTGACGGAAGAGCTTGACGACGAAAAGCTGGCGGATATC
CTGCAGGAATTGTCCGAGGACCGCCAAGCCGAGTTGATTGAAGAATTAGACATCGAACGT
GCCGCGGACATTCTGGAGGAAATGGATCCAGATGATGCTGCAGACTTGTGGGTGAGCTG
CCTGATGACAAAGCTGATGTGTTGTTGGATCTGATGGACCCTGAGGAATCTGCGCCGGTG
CGTCGTTTGATGGATTCTCCCCGGACACCGTTGGTGCGCTGATGACTCCTGAGCCATTA
ATTATGGATCCTTCCACCACAGTCGCTGAAGCGTTGGCGATGGCCAGAAACCCGACCTT
CCTACTTCTTTGGCATCGTTGATCTTTGTGGTGCGCCACCCACGGCCACGCCTACTGGA
AAATACCTCGGCTGCGTGATCTGCAGAACTGCTTCGGGAGCCTCCATCAAGTTTGATT
GGTGGCATCCTCGACCCCGATCTGCCACCGCTCTACGCTGATGATTCTCAAGAAACCGCA
GCTCGATTCTTTGCCACCTACAACCTGGTGTGCGGCCCGCTCTGGATGAAAACCGCCAT
CTGCTTGGTGCCGTAGCTGTGATGACTTGCTCGACCACATGCTGCCAGAAGACTGGCGC
GACGCCGAATCCGACCAGGAAAGGAGCACACCCATGGC

>RXA02068-downstream
TGATTTCACCGCTCTGAATTAG

>RXA02079-upstream
CGGGGAGCCGTGCGGACGCTGCGGAACATTAATCATCCGGGAGAGTTTCATGAACCGCGG
CTCCCCACTACTGCCCAAACCTGCCAGAAGCGGCGCTAGCTG

>RXA02079
ATGAGCGAAGCTTTTGATGCAACCAAAGTGCGCAAAGCTGTGCTCACCGTCGCGCTGCTT
AACTTCGCTTATTTCTTTGTAGAATTCTTTATTGCATTAAGCGCAGGCTCCGTTTCTCTA
CTGGCTGACAGTGTCGATTTTCTTGAAGACACCTCCATCAACCTGCTCATTTTCATTGCC
CTAGGATGGCCGTTGGCGAGGCGCGCAGTGATGGGCAAACCTATGGCGATTGTGATTCTT
GCACCTGCTGCTTTTGCTGCGTGCGGAGCGGATTCAACGGTTTCCGCACCGCAAGCGCCC
GAAGTGTTTCCGATCATCGTCGCTTCTCTGGGCGCCGTCGTGATCAACGGCGCGAGTGCC
ATCATTATTTCTCGAGTGCGACAACATGGTGGCTCGCTTGGCCAAGCTGCCTTCTATCC
GCCCCAAATGACGTCCTGATCAACATTGCCATCATCATGATGGCCTTAATTACCGCATGG
ACGACGTCTGGATGGCCAGATTGATCCTAGGTTGTTTCATCATTTCTGCTCGCACTGCAC
GCCGCTCACGAGGTGTGGGAAGTCAGTGAGGAAGAAGCCTCGCCTCCAAAGCCCTTGCT
GGGGAAGCCATCGAT

>RXA02079-downstream
TAGGGGAGCAGTATGAGCTTTTC

>RXA02096-upstream
CGCTTCGACGACCTACCCACAGCGATATCCGCAGGAATCTCATCGCGGTTTTTGATGAG
CCGTTCTTGTAATCCTCCTCCATACCGCGAGAACATCTCG

>RXA02096
ATGGGTTTGGATGTGATGAGCAGATCGAACACGCAGCCAGGCTTGCCAGGCTCAT
GATTTTATCGATCGCCTTCCAAACAAATACGAGGAAGTCATTGGCGAACGCGCCTGACG

CTTTCTGGTGGTCAACGCCAACGCATCGCCCTCGCACGGGCTTTCCTGGCGCATCCCCAA
 GTGTTGGTGCTTGATGATGCCACCTCTGCCATTGATGCCTCCACTGAGGACCGCATTTTC
 CAGGCCTTGCGCGAAGAACTGCACGATGTCACCATTTTGATCATCGCGCACCGCCACTCC
 ACTTTGGAGCTCGGCGATCGGGTTGGTCTGGTCTGAAGATGGACGGGTAACAGCACTGGGA
 CCGTTGAGTGAGATGCGTGATCACGCTCGTTTCTCGCATCTGATGGCTCTTGATTTCCAG
 GATTCTCACGATCCGGAATTCACCCTCGACAACGGTTCCTACCCAGCCAAGAGCAATTG
 TGGCCGGAGGTCTCCACAGAAAAGCAGTACAAGATTCTTGCGCCTGCCCCCTGGTTCGAGGC
 CGTGGCATGTCCATGCCAGCAACCCCTGAGCTGCTCGCCAGATTGAGGCGCTGCCAGCA
 GCAACGGAAGAAACACGAGTTGATGCCGGGAGGCTACGCACCAGTACCTCCGGTTTCAA
 TTGCTCAGTTTATTCAAGCAGGTCCGTTGGCTCGTCTGTCGCGGTTCATCGCGTTGTTGCTG
 GTGGGCGTAGCCGCCGATCTAGCATTTTCCAACACTGATGCGCGCAGCCATCGACAACGGT
 GTGCAAGCACAAGCACCTCCACGTTGTGGTGGATCGCCATCGCAGGCAGCGTAGTAGTC
 CTTCTGTCTTGGGCCGCCGCCGCGATCAACACGATTATCACGGCACGCACCGGTGAACGG
 CTGCTTTACGGCTTGCGTCTGCGCTCATTTGTGCATCTATTGCGCCTGTCCATGAGCTAT
 TTCGAACGCACCATGTCCGGCCGATCATGACGCGCATGACCACCGACATCGACAACCTC
 TCGTCCTTCCATCAAGGTCTGGCGCAAACAGTTGTCTCTGTGGGCACGCTCATCGGT
 GTGGTCACCATGCTCGCCATCACCGACGCACAACCTAGCACTCGTTGCGCTGTCCGTGGTG
 CCGATCATCATGCTGCTCACTCTCATTTTCCGACGCATCAGCTCCAGGCTGTACACCGCT
 TCACGCGAGCAAGCCAGCCAGGTCAACGCGGTATTCCACGAGTCCATCGCCGGTTTACGC
 ACCGCGCAGATGCACCGCATGGAAGACCAAGTCTTTGACAATTATGCGGGCGAAGCA

>RXA02119-upstream

TTCCGGTCCGCTCTGGCAAAAATGGCTGGCTGCCACCTCGGCGCAGCAGCTTAAGGGCTGG
 GCTTAAATGCTTGTTCGACGCCTAGTGCCACAATGGAGAC

>RXA02119

ATGACCGAAACACTTGTGGTGAATGGCCTTGACGGCGGCTATGGGCACCGCACATTATTT
 AACGATGTGAATCTCACCGTAGCTGCCGGCGATGTCGTGGGCGTTGTTCGGCGTCAATGGC
 GCTGGTAAATCCACATTTCTAAAAATCTGGCGGGCGTGGAAGCCACTGGCTGGAAC
 ATCGCGCTTTCCGCCAGCGATGCTTTTGTGGGCTACTTGCCACAGGAACACACCCGACG
 TCTGGAGAGACGATCGCAGTTTACATTGCTCGTGAACCGGCTGCCAAGCTGCAACAAC
 GCCATGGATGACACCGCCGAAGCGTTTGGTGGGATCCAGACAACGCTGCCTTGGCCGAT
 GCATACGCCGAGGCGCTGGATCGGTGGATGGCCAGTGGCGCAGCCGATTTGGATGAACGC
 ATCCCCATCGTGCTCGCTGATTTGGGCTTTGAGCTTCCCACCTCGACGCTGATGGAAGGA
 CTTTCAGGCGGGCAGGCAGCCCGGTCGGGCTGGCGGCGTTACTGTTGTACGTTTTGAC
 ATTGTGCTTCTCGACGAGCCCACCAACGATTTGGATCTCGACGGTCTTGAGCAACTGGAG
 AATTTTGTTCAGGGGCTTCGCGGGGGAGTCGTACTGGTCAGCCATGATCGTGAGTTTCTT
 TCCAGGTGTGTGACCACTGTGCTGGAACCTGATCTGCACCAAAATTCCCACCATGTTTAT
 GGCGGTGGATATGATTCCTACCTTGAGGAACGCGCAGTGCTACGCCAGCACGCCCGTGAC
 CAATATGAGGAATTTGCGGAAAAGAAGAAGGACCTTGTGGCACGTGCTCGAACGCAGCGT
 GAATGGTCTAGTCACGGTGTCCGCAATGCTATTAAACGTGCACCTGACAACGACAACTT
 CGGAAGAAAGCCGCTGCGGAATCCAGTGAAAAGCAGGCTCAAAAAGTCCGCCAGATGGAA
 AGCCGCATCGCTCGGTTAGAAGAAGTTGAAGAGCCACGTAAAGAATGGAAACTGCAGTTC
 AGCGTCGGTAAGGCGTCGCGGTCAAGTTCTGTTGTTTCCACGTTGAATGATGCAAGCTTC
 ACCCAAGGCGATTTACCTTGGGACCAGTATCCATCCAAGTAAATGCTGGCGATCGCATT
 GGCATCACAGGACCCAACGGTGTGGTAAATCCACATTGCTGCGCGGACTATTGGGAAAC
 CAAGAACCCACAGCGGTACTGCCACGATGGGCACGAGCGTGGCGATCGGAGAAATCGAT
 CAGGCACGAGCGTTACTTGATCCACAGTTGCCACTGATTTCTGCGTTTGAAAAGCATGTT
 CCAGACTTACCGATCAGTGAGGTGCGCACACTGCTCGCGAAATTTGGGCTGAATGATAAT
 CATGTGGAACGGGACGTCGAAAAGCTATCTCCTGGCGAGCGCACGCGCGCCGACTTGCG
 CTGCTACAGGTGCGGGGCGTCAACGTGCTTGTCTTGATGAGCCACCAACCACCTTGAC
 CTGGAGGCCATCGAGCAATTGGAGCAAGCGTTGGCCTCGTATGATGGTGTGTTGCTGCTG
 GTCACGCACGATCGTCGATGTTGGACGCTGTGCAGACCAATCGTCGTTGGCATGTTCGAG
 GCTGGCGAAGTTAGGGAGCTA

>RXA02119-downstream

TAACCGTTTCCGTATTGATGCCA

>RXA02220-upstream

GGGCTTTCGCCGCGGAATGGTCCCTCGTCCAGGTCTTTAATTGATGTCTTGACGTGATCT
 GGGCGGGCACGCGGCCAATCATGTGAAAGGTCTGT'TTTAG

>RXA02220

GTGTCGTCCCCTCTCCCCGCTGCCGTACATCAAAACCCGCCCACGCGCTTTCTCTGAT
 GAGGTGTTAGAAAATCTCGGGGTCCAGGACACCGGATTGACCTCCGCGGAGGCAACACAG
 CGTTTGGAAGCAAACGGGCCAAACGAGCTTCTCAAACCTCCACCTGAAACAGTCTGGCAA
 CGGCTATTCGCGCCAGGTCAACGATCCAATGATCTACGTTCTCATTGCCGCGCGGTACTC
 ACGGCGTTTCTTGCGCATTTGGACAGACACCATCGTGATCGGCGCCGTTGTCATCATCAAC
 ATGATGGTTGGGTTTCATCCAAGAGGGCAAAGCTGCGGATGCGTTGGCATCGATCCGCAAC
 ATGCTCTCCCCGGAATCCGCGGCGTTGCGCGATGGGGTCTTCCACAAAATGATGCGGCA
 GAGCTGGTGGTTCGGTGACGTTGTGAAACTATCCGCGGCGGATAAAGTGCCCGCTGACCTG
 CGCATGCTCGCCGCCACCAATCTGCACATTGAGGAATCCGCGCTCACCGGCGAGGCGGAA
 GCAGTGGTCAAAGGTACTGATCCAGTTGAGGCCGACGCGGGAATCGGCGACCGCACATCC
 ATGGCGTTTTTCAGGAACGCTGGTGCTCACAGGCAGCGGCACCGGCGTGGTCACCGCCACC
 GGTGCAGGCACAGAAATCGGGCACATCACCACCATGCTTGCCGACGTCGACTCCGTGGAT
 ACCCCATTGACTCGGTTCGATGAAAAAGTTCTCATCGGCGTTAGCAATCGTGTGTGTATTC
 CTAGCGATCCTCATGCTGGTGGTTGCCGGTCTAGTCCACCACACACCTTTGGAAGAGCTC
 ATTCTTTCCGCCATCGGCTTTGCGGTGGCTGCCATTCCGGAGGGTCTACCTGCGGTTATC
 GCCATCACGCTGGCATTTGGGTGTGAAAAGATGGCAGCTCGAAATGCGATTACGCGCCGG
 TTGAATTCGCTGGAAACACTTGGCTCTGTACCACCATCTGCACGGATAAAACCGGCACA
 CTCACCCGCAATGAGATGACAGTCCGCGCAATCGCCACCGGTACGAGTCTTTATGACGTC
 AGTGAGCAGGCTACGAACCTCTCGGGGAAATCCGCTTAAAAGACGGCGAGCAAGTATCC
 AAGCAGGATTTCCAGATCTCTACGCCATGGCGTTGGTCGCAGCGAACGTCAACGACGCC
 GAAATTTACCAAGAAGACGGCATGTGGAGGCTTTCCGGCGAACCCACCGACGGCGGTATT
 CGTGCCCTTTCGAATGAAAACCAACGCTGAAATCTTGACCCGAACAGCCGAAGTCCCCCTC
 GATTCCGCATACAAATACATGGCGACGCTTACACCATCGATGGAGCAAACACCATGCTG
 GTCAAGGGCGCTCCCGATCGTTTTATTTGGATAGAAGTGACAGCAGCGCAACGGTGAACCA
 CTTGACCGGCCGTATTGGGAACAGCTCATCGAGGACCTCGCGTCCCAAGGCCTCCGCGTG
 CTGGCTGCGGCATATAAAGAGCTTCCCCACAGCACGTCAACAATTACTCCAGAAGATGTT
 GACCAGGGCGAACTCACCTTCTCGGGCTCTACGGCATCATGGATCCGCCACGCGAAGAA
 GTCATCGAAGCCATGAAAGTGGTGCAATCGGCAGGCGTTTCGCGTCCGCATGATCACCGGC
 GATCACTCCTCCACGGCCCGCGCAATCGCCCGGAAGTGGGAATCCGCGGCCAGAACGTG
 CTCACCGGTGCGGAAATTACTGCGGCTACTGATGAGGAGCTGCAGGGACTCGTCGATAAT
 GCTGATCTTTTTGTGCGCACCAAGCCCCGAGCACAAGCTGCGCGTCTGCGCGCACTGCAA
 GCTAACGGCGAAGTCGCGTCCATGACCGGCGACGGCGTCAACGATGCGCCAGCGCTAAAA
 CAAGCCGACGTCGCGCTCGCCATGGGCATTAAGGGCACCGAAGCCACCAAGACGCGGCC
 GACATCGTGCTTGCCGACGACAATTTCCGCCAATCGCCGGCGCCGTAGAAATGGGTGCG
 ACCATCTACGACAACCTGCGCAAAGCCGTCGTCTTCATGCTCCCCACCAACGGCGCCCAA
 GGCTCGTCATTTTCATCGCGATGCTGCTCGGCTGGGAATGCCCATCACCGCACTTCAA
 GTGCTGTGGATCAACCTCATCACCGCCATCACACTGTCCCTGGCGCTGCTCTTCGAGCCG
 GCCAGCCCCGGCATCATGAACGAGAAACCCAGAAACCCCAAGAGCGGGCTTATCGACGCC
 CCTCCGCTGCTTCGCATCGTCTATGTCTCCCTGCTGCTCGGCGGAGCAACGTTCTGGGCT
 TTCTTGGCGCCCGGACGCGAGGAATCGACATCGACACCGCCCGCACCATCGCGGTACCC
 ACCCTTGACGTCAGCCAAGTGTCTACCTTTTAAGCTCCCGATACTTCGAAGTATCCGCG
 CTGCGAAAAGAACTCTTACCACCAACCCGATTTCTTGCTGTGCATCGCACTCATGCTG
 ATCCTGCAACTGGCCTTTGTCTACCTGCCGTTTCATGCAAAGCACCTTCGACACCGCCGCA
 CTGACGCTTAGAGATTGGGTTCATGCCACTGGTGTGTTGGTGTGTTGTCTTTGCGGTGCTT
 GAAACCGAGAAATTCATCAGGCGCCTTAAAGCGTCT

>RXA02220-downstream
 TAAGGTTTTAGCCCCCTCAAGATA

>RXA02222-upstream
 CATCCGCTGAACATCGTCTGTCTACAGCGTTTGGAGAACGCGAAAAAGATGAGGCAGTAC
 AAGATTGCAAAAACCTTGAAAAAGTGTATGGCAGCGATGG

>RXA02222
 TTGGGTGACCTCCCCAGGAGACGTTCTACTCTCCTAGACGATATCGGAGCAGAGGAA
 TCTGAAGCAGATAAAGTTCCAAATTGAATGGCAAAACGCCCTGACTAAGGCAGACAGGTAT
 GCAAACCGGCAACACATGTCTCAGGCACGACTCTATCGCCAATTAACCAGTGATGTTGGA
 GAGGGCTTCACTGAAGAAGCTGCCCAATACGCAATCGAAAATGTGAACGCAGACTGGAAC
 GCTAACGCCCTAGTAAAAGCAAGAAATTACCAGGAGCGCCAAGCAATGTCAGTAGACCGC

ATTACAGGCAACTTACTAGTGAACACGGTGAAGGGTTTACCCAGAGCAGGCACAATAC
GCGATCGACAACCTA

>RXA02222-downstream
TAAGGCATAAAGATCCTAGTATT

>RXA02312-upstream
TTAGCGCCCATTAACGCTTCACATCCTTATATTCCCAAGGAGCACGACCATTCTGATTC
AGCAGTCCAGGAGAATCACGAACCGCACCTCAAGCGCGGT

>RXA02312
TTGAGCAATAGACACCTTCAGCTCATCGCCATCGGCGGAGCGATCGGTACGGGTCTGTTC
ATGGGGTCCGGCAAGACGATCTCCGTTGCGGGGCCATCAGTAATTTTGGTGTACGCCATT
ATTGGTTTCATGCTTTTCTTCGTCATGCGTGCCATGGGAGAGCTGCTGCTCGCCAATTTG
AATTACAAATCTTTGCGCGATGCGGTCTCTGATATTTTGGGTCTGGCGCAGGTTTGTGTC
ACCGGCTGGACATATTGGTTCTGCTGGATTGCCACAGGCATGGCGGACATCGTGGCGATC
ACTGGATACACCAATACTGGTGGCCTGAGATCCCATTGTGGCTTCCAGGTGTGCTCACC
ATTGCGTTGCTGTTTGGCCTGAACCTGGCTGCGGTACGACTGTTCCGGTGAGATGGAGTTT
TGGTTCGCCATCATCAAAATCGTGGCTATCGTGTCTTGATCGTCTGGGACTTTTCATG
GTGGTCACAGCCTTTGAATCACCTAATGGCACCACCGCGCAGTTCAACAACCTCATGAG
CATGGCGGATTTTTCCCCAACGGCATCACCGGTTTCTTGGCTGGTTTCCAGATCGCTATC
TTTGGCTTCGTCGGGATTGAACCTTGCCGGCACTGCAGCTGCAGAGACTGAGAATCCCACC
AAGACGCTTCCTCGGGCAATCAACTCCATTCCCATCCGCATCGTGGTGTCTATGTTTGTG
GCGTTGGCTGTGCATCATGATGGTCACCCCATGGGATCAGGTCCGTGCTGACAACAGCCCA
TTCGTGCAGATGTTTCGCGCTGGCAGGAATCCCAGCGGCGGCAGGCATCATTAACCTTTGTG
GTCATCACTTCTGCAGCGTCTGCTGCCAACAGTGGTATTTTCTCCACCTCCCGCATGTTG
TATGGATTGTCTTTGGAAGGCGCAGCTCCGAAACGGTGGAGCCGGTTGTCCAAGAACTTG
GTGCCAGCCAGGGGATTGACTTTTTCTGTGATTTGCCCTCATTCAGCGGTGGGTTTGTGCTG
TACGCTGGCGGCACTGTGCATCGAGGCATTCACACTGATCACCACGGTTTCTTCGGTGTG
TTCATTGGTGGTGGTCTTACATTTTGGTGGCTTATATCGTCTACCGCCGCAACAGCCCG
GAATTACACAAAAAGTCGATTTTCAAAATGCCTGGCGGCGTGGTTCATGGCAGTTGTGGTG
TTGGTGTCTTCGAGCGATGTTGGTGGTGTGCTGCTCCCTGGAGCCGGATACCCGTGCAGCG
CTCATCGCGACGCCAGTGTGGTTTCATCATTTTGGGTATCGGTTGGTTGTCCATCGGTGGA
GCTAAGGGCGCTAAGCATCGCAGCCAAATAACCTCCCAC

>RXA02312-downstream
TAAAGCTCCTGGGTTAGACTCGA

>RXA02313-upstream
CAGGATGTAACCGAAAAGATCTCAACACTTAAATAAAGTTCTCGATAAAGCCATGTTCCGG
TTAACTGCGATGTAGGCATGATGTGGAGATAATAAGGCC

>RXA02313
ATGCGGGTAGCAATTGTTGCAGAGTCGTTCTTCCAAATGTCAACGGAGTCACCAACTCG
GTGCTCCGGGTGTTGGAGCATTTGAAAGCCAACGGACACGACGCGCTCGTCATCGCGCCG
GGTGCCCGGGATTTTGAAGAAGAAATCGGCCACTACCTGGGCTTTGAAATTTGTGCGCGTC
CCCACCGTTCCGGTCCCAGTATTGATTCACTGCCCATCGGTGTTCTCTGCCCTCAGTT
ACCTCTGTGCTGCGCGAGTACAACCCAGACATCATTCACCTGGCATCCCCATTGTGCTC
GGTGGAGCGGCAGCATTCGAGCAAGGCAGCTGCGCATCCCAGCAATTGCTATCTATCAA
ACTGATGTGCGAGGGTTCTCCAGCGCTACCACCTGGCACCGTTGGCCACTGCAAGCTGG
GAATGGATCAAGACGGTCCACAACATGTGCCAGCGCACCTTGCTCCCTCATCCATGAGC
ATTGACGAGCTGCGTGACCACGGAATTAATGATATTTTCCACTGGGCTCGGGCGTGGAC
TCCAAGCGTTTCCACCCTGGAAGCGTTCCGTAGCGCTACGTAAGTCTTGGGATCCCAAGT
GGAGCAAAGAAGATCGTTGGTTTCGTTGGGCGCCTTGTCATCCGAAAAGGGCGTGGAGCGC
CTTGCTGGATTATCCGGACGCTCAGACATCCAATTGGTCATCGTCCGTGATGGCCAGAG
GCCAAGTACCTGCAGGAATGATGCCGGATGCGATCTTACAGGAGCTCTCGGCGGCGAG
GAACTAGCCACCACCTACGCATCACTCGATCTGTTGTGCACCCAGGTGAGTTTGAAACC
TTCTGCCAGGCGATCCAGGAAGCCCAAGCATCAGGTGTGCCACCATTTGGCCACGCGCA
GGTGGTCCCATTGATTTGATCAACGAAGGCGTCAACGGCTGCTTCTTGATGTTGTAGAT
TTCAAGGAACCCCTCCCGCTGCAGCCGAATGGATTTTGGACGATTCCCGCCACTCCGAA
ATGTGCGCAGCTGCTTGGGAAGGTGTGAAAGACAAGACCTGGGAAGCTTTGTGCACCCAG

CTTCTCCAGCACTACGCGGATGTAATCGCATTGTCACAGCGCATCCCACTGACATTCTTT
GGCCCTAGCGCTGAAGTAGCAAAGCTTCCACTGTGGGTGCTCGCGCGCTGGGTGTTTCG
ACCCGCATCAGCATCGAGGCT

>RXA02313-downstream
TAACTCTGCAGAAATTAATCCATG

>RXA02344-upstream
AAAGACCCGAGCCGAAGCCCTGGCCTGCGCATACTTCCTTGTCACGCTCGCTGGGATTA
GGTCTTTTCTGAGCGCTAGCATTTCTCCACTCAAAGGAGC

>RXA02344
ATGCTTAACCGCATGAAAAGTGCGCGGCCAAAATCAGTCGCTCCAAAATCCGGACAAGCT
TTACTCACTCTCGGTGCCCTAGGTGTTGTGTTTCGGCGACATCGGCACCAGCCCCCTGTAC
TCACTTCACTGTCATTGAGCATGACAGACAACAAAGTCGAAGTCACTCAGGAAAATGTG
TACGGCATCATCTCCATGGTGTGTTGGACCATCACTTTGATCGTCACCGTCAAATACGTC
ATGCTGGTCACCCGAGCTGACAACCAAGGACAAGGTGGCATCCTGGCGCTCGTTGCTTTG
CTGAAAACCGTGGGCACTGGGGAATTCGTGGCAGTAGCCGGCATGTTGGGCGCCGCA
TTGTTTTATGGCGATGTGGTGATCACCCCGCGATCTCTGTTCTCAGCGCAACAGAAGGC
TTGACGGTTATCTCCCCAAGCTTTGAGCGCTTCATTCTGCCCGTATCTCTCGCAGTTCTG
ATCGCTATTTTTGCAATCCAACCGCTCGGTACAGAAAAGTCGGCAAAGCCTTCGGCCCC
ATCATGTTGCTGTGGTTTTGTACCCCTTGACAGGATTGGGAATTCGCAAATCATCGGGCAC
CCAGAAATCTTGACAGAGCTTGCTCCACATTGGGCCCTGCGCTTGATTGTGGCTGAGCCT
TTCCAAGCATTTGTGCTG

>RXA02348
CCAATCAGAGTGGCGTGGTTTTGCGTCGTCATGCCTGCTTTAATCTTGACGTATTTGGGG
CAGGGCGCCTTGGTGATCAACCAGCCTGAAGCGGTGCGCAACCCCATGTTTTATCTCGCG
CCGGAAGGTCTGCGGATTCCGTTGGTTATTTTGGCGACCATCGCTACGGTGATCGCATCG
CAGGCCGTGATTTCTGGTGCGTATTCAATTGACCAAGCAGGCCGTGAATTTGAAACTGCTG
CCACGCATGGTGATCCGGCATACTCCCGCAAAGAGGAAGGCCAGATCTATATGCCACTG
GTTAATGGATTGCTGTTTGTATCCGTGATGGTTGTGGTGCTGGTATTCCGATCCTCTGAA
AGCCTCGCCAGCGCTACGGACTTGACGTGACCGGAACCTTGGTGCTGGTCAGCGTCCTG
TATCTGATCTATGTTACACCACATGGTGGAACAGCGCTGTTCAATTGTGCTCATCGGT
ATTCCAGAAGTACTTCTATTGCGCTCGAACACCACGAAAATTCACGACGGTGGCTGGCTT
CCACTACTTATTGCGGCCGTGCTCATCGTGGTGATGCGGACCTGGGAGTGGGGAAGTGAC
CGCGTCAATCAGGAACGCGCAGAGCTGGAACCTCCCATGGATAAGTTCTTGGAGAACTC
GATCAGCCACACAATATTGGTCTGCGTAAAGTTGCCGAAGTGGCAGTATTTCCACATGGC
ACCAGCGATACTGTCCCGTTGTCAATTGGTTGCTGCGTGAAAGACCTCAAGCTTTTATAC
CGAGAGATCGTGATCGTTTCAATCGTCCAAGAACACGTTCCGCACGTGCCACCAGAGGAA
CGCGCGGAATGGAAGTGCTCCATCACGCCCCGATCAGAGTCGTGCGAGTTGATCTGCAC
CTTGGTTATTTTATGAGCAGAACCTGCCTGAGCATCTCCATGCCATTGACCCAACATGG
GATAACGCCACCTACTTCTGTCTGCCCTGACTCTTCGGAGCAGGTTGCCTGGAAAGATT
GCTGGCTGGCGTGATCGTTTGTATCTTTCGATGGAACGTAATCAGGCATCTCGAACTGAG
TCTTTCAAATTGCAACCAAGCAAACCATCACGGTTGGAACAGAGCTGCACCTT

>RXA02348-downstream
TAATCAGGCAGTTGCTGGCCAAC

>RXA02353
ATGGCACTGCTGATCCTCGCCGGTCTGCAAATGATCCCGAAGGAAACCTACGAAGCAGCC
CGCGTCGATGGCGCAACCGGTGGCAGCAATTACCAAGATCACCTCCCGCTGGTGCGC
CCAGCTTTGATGGTGGCAGTACTCTCCGCACCCTCGATGCGCTACGCATGTATGACCTC
CCCGTCATCATGATCTCCAGCTCCTCCAACCTCCCCACCGCTGTTATCTCCAGCTGGTT
GTGGAAGACATGCGCCAAAACAACCTCAACTCCGCTTCCGCCCTTTCCACACTGATCTTC
CTGCTGATCTTCTCGTGGCGTTTCATCATGATCCGATTCTCGGCGCAGATGTTTCGGGC
CAACGCGGAATAAAGAAAAAGAACTGGGCGGAACCAAGGATGAGAAACCCACCGCTAAG
GATGCTGTTGTAAAGGCCGATTCTGCTGTGAAGGAAGCCGCTAAGCCA

>RXA02353-downstream
TGACTAAACGAACAAAAGGACTC

>RXA02354-upstream
GAATAAAGAAAAAGAACTGGGCGGAACCAAGGATGAGAAACCCACCGCTAAGGATGCTG
TTGTAAAGCCGATTCTGCTGTGAAGGAAGCCGCTAAGCC

>RXA02354
ATGACTAAACGAACAAAAGGACTCATCCTCAACTACGCCGGAGTGGTGTTTCATCCTCTTC
TGGGGACTAGCTCCCTTCTACTGGATGGTTATCACCGCACTGCGCGATTCCAAGCACACC
TTTGACACCACCCCATGGCCAACGCACGTACCTTGGATAAATTCCGGGACGCACTGGCC
ACCGACAAAGGCAACAACCTTCCTCGCAGCCATTGGCAACTCACTGGTCATCAGCGTCACC
ACAACAGCGATCGCTGTTCTCGTGGGAGTGGTCACCGCCTACGCTCTAGCCCGACTGGAA
TTCCCGGGCAAAGGCATTGTACCGGCATCATCTTGGCAGCCTCCATGTTCCCGGCATC
GCCCTGGTCACCTCCGCTGTTCAGCTCTTCGGTGACCTCAACTGGATCGGCACCTACCAA
GCGCTGATTATCCCGAACATTTCTTTCGCGCTACCTCTGACGATCTACACGCTCGTATCC
TTCTTCAGGCAACTGCCCTGGGAATCGAAGAATCAGCACGTGTGACGGCGCCACACGT
GGCCAAGCCTTCCGCTGTATCCTGCTTCTCTAGCAGCGCCGCACTATTTACCACCGCG
ATCCTCGCATTCATTGCAACGTGGAACGAATTCATGCTGGCCCCGCAACTATCCAACACC
TCCACAGAGCCAGTGACCGTTGCGATCGCAAGGTTACCGGACCAAGCTCCTTCGAATAC
CCCTACGCCTCTGTCATGGCAGCGGGAGCTTTGGTGACCATCCCACTGATCATCATGGTT
CTCATCTTC

>RXA02394-upstream
TGTTGATGAATCAGAAGAACCTCGAGATTTGGACGAGCTAGAGGCCCAAAGCGCTATAGA
TTCTGCAAGTTCAGCGGAAGGTAGGAACATAAT

>RXA02394
ATGTTGTGCGCCAGCAGCTGTAGCAGCTTTAATTCTTGTATCGGCATTGTGGTGCTCATC
ATCGCATCAGTGCCCGTTGCCATTGCCATCGGTTTGCCATCACTTTTTGCCGCGATGGCC
GTGCTTGGCCCAGAAAACGCCGCGCAGGCCGTCGCGCAGCGCATGTTTACCGGCACAAAC
TCCTTTTACACTCCTTGCCATTCCGTTCTTCGTGTTGGCGGGTTTGTGATGAACCTCGGGT
GGTATTGGCAGCGCGCTTATCGACGCCGCGAAGGTGCTTGTGCGCCGCATGCCTGCCTCC
ATGGCCAATACGAATATCGCAGCAAATGGTCTCTTCGGAGCAGTTTCAGGGGCAGCGGTA
GCATCAGCTTCTGCCGTGGGAACCGTCATGACACCAAAAATGAAGGAAGAGGGCTACTCG
CGCGCTTACGACGCGCGCTCAACGTGGCTTCAGCACCTGCGGGCATGCTGATCCCGCCA
TCAAACACTTTTATTGTGTATTCTTGGTGCTCTCGACATCAATTGCAGCACTATTTATG
GCCGGTGTGGACCCGGTCTGCTCTGGATTCTGGCCTGTGTATCGTGGGAACCTGGTTA
GCGCGAAAGGAAAACTACAAGCGCGAGCAGATTCAACCAATTCAAGCAGTCGCTCGTT
GTGCTGTGGAGGGCGCTGCCTTCACTGCTCATGATCGTCATTGTTGTTGGAGGTATCTTG
CTGGGCTGGTTCACTCCAACCTGAATCCGCTGCTATTGCTGTAGTGTACTGCCTGGTCTTG
GGCTTTATTTACCGCACAAATCAAGGTGGGAGATCTGGCAGATATTTTGCTCAAGGCAACT
CGCACCATCAATTGTATGTTGCTCATTGCAGTTTCTGCAGCACTGTCGTGGGTGATG
GCCTTTGCAAGATCCCTCAGATGATCTCTGATGCGCTTCTTTCCGGTATCCGATTCCAAG
GTTGTATCTTGTGATCATGATGTTTCATCCTGTTACTCATCGGTACCGTAATGGACCCA
ACACCAGCAATTTTGATCTTCGTCCCGATCTTCCTTCCAGTGGTTACCGAACTTGGTGTG
GACCCAGTCCACTTCGGTGCGATGGTGGAATGAACCTGTCCGTGGGCGTGATTACCCCA
CCAGTAGGCAACGTGTTGTTTCGTTGGTTTCGCAAGTGGCAGGGCTGCGTGTGGAACTGTG
ATCAGACGACTGTGGCCGTATCTCATTGCCATTATTGTTGCGCTGTTCTGTGGTTGTTTTT
GTACCGCAGATCTCTATCTGGCTGCCACAACAATGGGATTGATGGGAGGC

>RXA02394-downstream
TAAACCTCCAGCCATCAGCTAAG

>RXA02402-upstream
CACTACTGCGTTAAGGTATGAAAGTTTCGCACACCAGCGATTTAATTCTGTGCCACCCT
AGCACGACCATTTCAGTTTTAACTTTCTTGGAGTTTTCTA

>RXA02402
GTGTCCAAAAACAGAAGAAGGCCGTTTCAGCGGCCATAATTATTTACGCGTTTCCAACCTTC
ATTCTGTGGGCGCGATCATTGCGTTTATCTTCCCGGAACCATTCATTCCGCTGACAAAC
TACATTAATATCTTCTCAGATCATCATGTTACCATGGGTTTGACCTTGACGGTGCCC
GATTTTCAGATGGTGCTTAAACGTCCACTGCCTATCTTGATCGGTGTAGTAGCGCAGTTT

GTCATCATGCCATTCTGGCGATCGTGGTTGCGAAAATGTTCAACCTCAACCCAGCACTC
 GCCGTTGGCCTTCTCATGCTGGGATCCGTTCCGGGTGGCACCTCCTCCAATGTGATTGCG
 TTTCTCGCCCGAGGAGATGTCGCGCTATCGGTACCATGACCTCTGTGTCCACCATTGTT
 TCCCCAATCATGACGCCTTTCTCATGCTCATGCTGGCAGGTACTGAAACCGCCGTCGAT
 GGTGGAGGCATGGCGTGGACTTTGGTACAAACAGTGTCTGCTGCCTGTGATCATCGGCCTA
 GTTCTGCGTGTCTTCTTGAACAAGTGGATCGACAAGATTTTGCCGATCCTTCCTTATCTC
 TCCATCCTCGGTATCGGTGGCGTGGTGTTCGGCGCAGTCGCAGCCAACGCGGAACGACTC
 GTGTCTGTCGGACTCATCGTGTTCGTTGCAGTTATCGTGCACAACGTACTTGGATACGTT
 GTGGGATACCTCACCGGCCGTGTA

>RXA02422-upstream

CTTAAACGTACCTTATTTATGCATTATGTTGGTTTCAGACTCGAACAATTCAATTAGAA
 AACACTAATCGGACATTTAGGTACATAACATTTCCGCTC

>RXA02422

GTGTCCACATTAATTTCTGAACCCGAGGTGGATAAGCTACGTAAACGTGCCAAGAGATCA
 AGGCGGACAGAATGGTGGCTTGCCGCCGCACTTCTTGCCCCAACTTGCTTCTCTTGGCC
 ATCTTTACGTATCGGCCACTGTTAGATAAATTCCGGTTGTCTTTTTCAACTGGAACATT
 TCCTCGCCACATCAACCTTCATTGGGTTTGATAACTACGTTGAGTTCTTCACTCGTAGT
 GACACTCTCCAAGTTGTTTTAAACACCGTCATCTTCACGGCATGTGCTGTGATCGGATCG
 ATGGTGCTCGGTTTGCTCCTGGCCATGTTGTTGGATCAGAAGCTTTTCGGCCGTAACTTT
 GTGCGTTCCATGGTGTGTTGCCCGTTTGTGATTTCGGGTGCTGCCATTGGTGGTGCTTTC
 CAGTTCGTTTTTGAC

>RXA02438-upstream

CAGGTTGGAACCTGACTGGTTCATGTTCTTCTCGGCGGCACCCTACTTCTGGCTGTTT
 TGCTCAATCACCGATTTCGAGCGTTTCAACAAGGAGCGATC

>RXA02438

ATGACAGACCTCATTCAACTCCGCGAAGTATCCAAAAATACGGTGCTTTCCAGGCCCTC
 AACGACATCAATTTGAACGTCCGCGCAGGCGAAGTCACCTGTGTTCTGGGTGACAACGGC
 GCCGGAAAAATCCACCCTCATCAAGATTCTCTCCGGCCTGCATCCCGCCACCTCCGGCGAA
 GTAATCGTGGCCGGCGATGTAGTGAATTTGGATCCCCCGCGACGCCCTCGACGCCGGA
 ATCGCCACCGTCTACCAAGACCTAGCAGTGGTCGGGCAGATGAGTGTGTGGCGCAACTTC
 TTCTCGGCCAGGAACCTACCGGCCGATTGCGGTTCTGAAACAAGAAGAAATGCGCCGC
 ATCACCAGCAACAACCTCCGCGAAATGGGCATCGAACTCCGCGATGTCGACGTCCCTGTG
 GCCTCCCTTTCAAGTGGTCAACGCCAAGTTGTGCGCATCGCCCGCGCCATCTACTTCGGC
 GCGCGCGTCCCTCATTTTGGACGAGCCCACCGCAGCGCTGGGCGTGAAACAATCTGGCATG
 GTGCTGCGCTTTATTGCCGAGCAGCGACCGGGGGATCGGCGTCATTTTCATCAGCGAC
 AACCCCCACCGCCTACCTTGTGCGGTGATCACTTCATCCTGCTCAACTTAGGCAAGCAG
 GTCATGGACAAAATCCCGCGCAGAAGTCGAGCTGGAAGAACTCACCTCGCCATGTCCGGC
 GGCGGCGAGCTCGACTCACTCAGCCACGAATTGAAGCGT

>RXA02438-downstream

TAACCTACTTCTTCTTTTCGCTC

>RXA02439-upstream

GCACCACTGTTGGTGGCGGACGACCCGTGTACACAGGACCAGCCATTGTGGATGCCACCA
 ACGTTGATGTCAATTGCTGAAGCCGTTGGGGAGGGTCTGCG

>RXA02439

ATGACAAAAATCAAGAGTGGGGAGGCGTCGACAAGCATTGTTGAGCGCGCCTTAAAGCGC
 CCCGAACCTGACCAGCCTGCTTGGCGCCGTGCTTGTGTTTTACGCTGTTTATGGTGGTTCGCG
 CCGGCATTTAGGTTCATGGGATTTCGATGGCGACCGTGCTGTATGCGAGTTCCACGATCGGC
 ATCATGGCGGTTGCCGTGGGCTGCTGATGATCGCTGATGAATTGACCTGTCCACCGGC
 GTTGCCGTGACAACCTGCAGCGCTGGCGGCTCGATGTTTAGCTATAACCTGTGGCTGAAC
 ACCTGGGTGGGCGCGCTGATTGCATTGGTGATTTCGCTGGCCATCGGCTTTTTCAACGGC
 TTTTTGGTAGGTGAAAACCAAGATTGCATCCTTCCTGATCACCTTGCCACTTTCCTTATG
 CTGCAGGGTATTAATCTGGCGGTACCAAGCTGATTTCCGGCACCGTGGCCACGCCAACC
 ATCGCGGATATGGAAGGTTTTCTTCAGCGCGTGCGGTGTTTGCCAGCTCGATTCCCATC
 TTTGGTGTGAATATTCGCATCACTGTTTTTGGTGGCTGCTGTTTGTATCGTCGGCACT

TTTGTGTTGTTTAAGACGCGCATCGGCAACTGGATTTTTGCGGTGCGTGGCGATGAAGAG
GCAGCTCGCGCAGTCGGCGTTCCCGTGCGTGGCGTGAAAATCGGCCTGTTTCATGTTTCGTT
GGTTTTGCCGCTGGTTTGTGGGCATGCACAACCTGTTCTCTTTGATTTCGATTACAGGCT
GGTCAAGGCGTGGGTAATGAGTTCCTCTACATCATCGCTGCGGTGATCGGAGGCATCTCC
ATGACTGGTGGCCGCGGAACAGTGGTGGGCACAATGATTGGTGCATCATCTTTGGAATG
ACCAACCAAGGCATTGTTTATGCAGGTTGGAACCTGACTGGTTCATGTTCTTCCTCGGC
GGCACCTACTTCTGGCTGTTTGTCTCAATCACCGATTTCGAGCGTTTCAACAAGGAGCGA
TCA

>RXA02439-downstream
TGACAGACCTCATTCAACTCCGC

>RXA02441-upstream
CCGGCGACAGGGCGCGGGAGATGAATGAAACGTCAAAGGCACTATGAGGGCGTCAGTA
AAAAACTTCATTTGAAAATGATAACCGTTATCATTAAGGA

>RXA02441
ATGGCAGAACTCAGCGTCCGGAATCTCACATGCACATACGGCAATCACATCGCGCTCAAC
AACATCACGGCAGCGTTCCCAACCGGAAAAATAACTGCCCTCATCGGCAGCAACGGCTCC
GGAAAATCCACACTGTTGGAACTTTGGCGGGCATGCTGGCACCCCGCAGCGGAAGCATT
AACAACTTGTGCCAGAAATCGCGTTTCGTCCCCAACGCAGCCACGTCTCCATAATTTG
CCCATCACGATCAGACAAACAGTCAGCATGGGGCGATGGTCAGCCAAGAAAACTGGCAA
CGACTCACTGCCGAGATTGCAACATCGTGGACAGCTGCCTCGACCGGCTCGAAATCTCC
GGCTCGCGACCGCCCCCTCGGCGAAGTATCAGGCGGGCAGCGCCAACGCGCCCTCATA
GCGCAAGGTTTAGCGCAACAGGCGCCCTTATTGCTTCTCGACGAACCCCTCGCCGCGGTG
GACTCCACGCGGCAAGTCTTATCGAAGATGTCATTAACCAACAACGCAACCAAGGAACC
ACAATTATTCTTGGACTCACGATCTTGATCAAGCACATCAAGCAGATCAGATTATCGCC
TTGAAAAAGGAATCATAAAGCCACAGCGCAAAGCCACTGAATCAATAAAGAAGCGT

>RXA02441-downstream
TAATAAAGTTTGACTTGTGCCTC

>RXA02442-upstream
GCCGTGATGTTGTTGAGCGCGATGTGATTGCCGTATGTGCATGTGAGATTCCGGACGCTG
AGTTCTGCCATTCTTAATGATAACGGTTATCATTTTCAA

>RXA02442
ATGAAGTTTTTTACTGACGCCCTCATAGTGCCTTTTGACGTTTCATTTCATCTCCCGCGCC
CTGGTCGCGGATGCCTGGCCGCAATTTTATGCTCACTCATTGGAACGTGGGTTATTTTG
CGCAGGCTAACCTTTTTCGGCGACGCTATGTGCGACGGCTTGCTCCCCGAGTAGCCACG
GCATCACTATTGGGCGGAAATCTCATGTTGCGGCGAGCAATCAGCGCATTAATCATGTCA
GCCGGAGTGGTGTGGACCAGCAGAAAATCCAGCCTCTCCAAGACGTGAGCATTTGGCCTG
CAATTTATTACCATGCTTTCCCTCGGCGTGGTTATTGTGTCCCACTCCGATTCCCACGCC
GTAGACCTCACCAGTTTCCTTTTTGGAGACATTCTTGGCGTGCGACCCCTCGGATATATTC
ATCATCGCCATTGCAACAGTGTGGGTGGATTGACTATTTTTCTCTTCCACCGACAGTTC
ACTGCACTCGCTTTCGACGAGCGTAAAGCTCACACCTTAGGACTCAATCCCCGCTTTGCA
CACCTACTCATGCTGGCACTGATCGCATTAGCTACGGTGGTGTGCTTTTCAGGTGGTGGGA
ACGCTTTTAGTGTTTGGACTTCTCATTTGGTCCGCCCCGCCACGGCTGCACTTTTAGTGCAA
GACAAAGCAAGTATTTCACTGATCATGATCGTCGCTCGCTTCTTGGATGCGCGGAAATT
TACCTCGGGCTTTTAATCAGCTGGCAGCAAGCACTGCCGCGGGAGCCACTATCACTTTG
TTAAGTGCTGCGATATTTTTTGCACCTTATTGACAAAGAGTGCCATTAGTAGGTTAAAC
TTCACCGCG

>RXA02442-downstream
TGATACTGAAAGACATTTTCAAT

>RXA02447
TGGGTGTGGCTGGCGGAAATCTTCCAGTCCGAATGAAGGTATCGGCACCGGTATTTTCG
GTATTCTGCGGTTGGGGCATCAATGGCGTCTAGCGTTGTTCTTCCAGCACTGGTCTCC
GGCGTGGGTATCACCTTCTCCTTCTTATCTTCGAGTCGTGCGAGTCATTGCCCTGGCG
TTCGTACCAAGTTTGTTCCTGAAACCCGTGGCCGCTCACTTGAAGAACTCGATCACGCA

GCATTACACGGCCAGATCTTCAAGAAGGCT

>RXA02447-downstream
TAAACCCCTCCGATCTCTTTGG

>RXA02451-upstream
GATCAACTTAAGCCTCTAGCTATTTTCAACTGTGTTTCAGTTGCGGGATCGTTGGGTGCC
TAATTGGAGTTGTGCTTTTAGGTGGAGGATCATAGAGGTT

>RXA02451
ATGAACACCGACACAACCTCAAGACGGTGTGAGTCCTGAACCTTCCGACCCCCACCTAGGG
TCTGAAGTGGCGGAACTCACCGCGAAAAGAAATTCTTCGGCCAGCCTTGGGGGCTGGCA
AATCTCTTCGGCGTGGAGATGTGGGAGCGATTACAGCTTCTACGGCATGCAGTCCATCCTT
GCTTTCTATCTGTACTACTCCGTACCGATGGCGGACTTGGTATGAATCAGACAGCTGCA
CTGTCCATTGTGGGCGCCTACGGCGGCTTCGTCTACATGACCTCCCTCGTGGCTTCGTTT
ATTGCAGACCGAGTATTGGGCTCTGAACGTACACTCTTCTACTCCGCGATCATCGTCATG
CTGGGCCACATTGGCCTGGCCTTGATTCCGGGATATACGGGACTGTCCATCGGCTTGGTC
CTCATCGGCCTTGGCTCAGGTGGCGTGAAGACGGCAGCGCAGGTTGTGCTGGGCCAGCTG
TACTCACGCACGGACACGCGTCGAGACGCAGGCTTCTCCATCTTCTACATGGGCGTCAAC
CTCGGTGGCCTCTTTGGCCCGCTGATACCAACGCTCTGTGGGGATGGGGAGGATTCCAC
TGGGGCTTCGGTATCGCCGAGTCGGCATGGCTTTGGGTCTCATCCAATACGTGGCGATG
CGTAAACCACCATCGGTGCGGCAGGCCATACTGTTCTTAACCCACTGCCTAAGAATGAA
TATGCGCGCTGGATTATCGGTGCAGTCGTGGTTGTGCGCAGCAGTTGTGCTCTCATCGCA
ACGGGCATCATCAAGCTGGAATGGCTGTCCAACATCACCGCAGCGATCGCACTGATTGCG
GCTATTGCTCTGCTTGTCTCAGATGTACGTTTCCCCACTGACCACCGCAGCGGAAAAGTCC
CGCTTGTGGGATTTCATCCCGATGTTTCATCGGTGGCGTGCTTTTCTTCGCGATCTTCCAA
ACCCAGTTCACGGTCCTCGCGGTTTACTCCGACACCCGCTGGACCGTAACCTTCTTCGGC
ATTGATCTTCTCCAGGATTGATCAACTCCTTCAACCCAATCTTCATCATCATCTTCTCC
GGAATCTTTGCCACCTTGTGGACAAAACCTCGGAGCAAAGCAGTGGTCTACTGCAGTGAAG
TTCGGTGTGCGCAACATTGTCAATTGGTTGCGCGCTGTTCTTCTTCTGCGGTTCCGCGGC
GGTGCAGAGAACTCTACCCCAATGGCACTGATCATTTGGGTCTACTTCTCTTACCATC
GCTGAGCTTCTGCTCTCCCTGTTCGGCAACTCACTTGCAACCAAGGTGCGACCCGAGGCA
TTCAGTCCCGCATGTTTCGCGGTGGCTGATGGCTGTCTCCATGGGTACGTCCCTGTCC
GGCACCTTGGGTGGTTACTACGATCCAACCGATGCAGGATCTGAAAAGGTCTTCTTCATT
ACCGTTGGCGTTGCAGCCATCGTTCTTGGTGCAATCGTCATAGCAGCCAAGGGCTGGGTG
CTGAAGAAGTTCATCGACGTCCGA

>RXA02451-downstream
TAGGCCTCACAAAGCCTCAAAAC

>RXA02491-upstream
TTTCGTATGTGACATGGTGTCCCTTCAACTGCGTTGCTTTAGTGCCCTTTAGTATATAG
AGACGTCCCGCTGCTTTCTTCGGCGATCTAGAATGTGGGC

>RXA02491
ATGCGCGTAGCTATGATTTCCATGCACACCTCTCCATTGCAGCAGCCCGAACTGGTGAT
TCAGGCGGCATGAACGTCTACATTCTTTGACCGCGACTGAGCTAGCGAAACAGGGTATC
GAGGTCGATATTTACACTCGTGCCACGAGGCCTTCTCAGGGTGAGATCGTGAGAGTAGCT
GAGAATTTGCGGGTCATTAATATCGCTGCGGGGCGTATGAGGGGCTTTCCAAAGAGGAG
CTTCTACTCAGTTGGCGGCGTTTACCGGCGGAATGTTGTGCTTTACGCGCCGGGAGAAG
GTTACTTATGATCTGATCCATTCTCACTATTGGCTGTCTGGTCAGGTGGGGTGGTTGCTG
CGCGATTTGTGGCGGATTCCCCTTATTCTACCGGCACACACTTTGGCGGCGGTGAAGAAT
TCTTATCGGGATGATTCCGACACTCCGGAGTCGGAGGCGCGTCGCATTTGTGAGCAGCAG
CTGGTGGATAACGCTGACGTGTTGGCGGTGAACACTCAGGAGGAGATGCAGGATTTGATG
CATCACTACGATGCGGATCCGGATCGGATTTCTGTGGTGTACCCGGGTGCGGACGTGGAA
CTTTATAGCCCTGGAAATGATCGCGCGACGGAACGTTCCCGTCGTGAGCTGGGCATTCCG
CTGCACACAAAGGTAGTGGCTTTTGTGGGTGCGTTGCGAGCGGTTAAGGGCCCGCAGGTG
CTGATCAAGGCGGTTGCGGCGTTGTTTGATCGCGATCCGGACCGAAATCTGCGCGTCATT
ATTTGTGGCGGCGCTTCTGGTCCGAATGCGACACCGGATACCTATAGGCATATGGCAGAG
GAACTGGGCGTCGAAAAGCGAATTCGCTTTTGGACCCGCGCCCGGAGCGAGCTAGTG
GCCGTGTATCGGGCGGCGGACATCGTGGCCGTGCCAAGTTTTAATGAGTCCTTCGGACTC

GTCGCCATGGAGGCGCAAGCCAGCGGCACACCGGTCAATTGCGGCCCGGGTTGGCGGCCTG
CCCATCGCAGTCGCGGAAGGGGAGACGGGATTGCTTGTGACGGCCACTCCCCGCATGCC
TGGGCCGACGCCCTTAGCCCACTCTTGGACGATGACGAAACGCGCATCAGAATGGGTGAA
GACGCCGTGCAACACGCCAGAACATTCTCCTGGGCGGCCACCGCCGACAGCTATCGTCG
CTGTACAACGACGCTATTGCCAACGAAAATGTGACGGTGAAACGCATCACGGC

>RXA02491-downstream
TAAGTAAACGCGCTCGTGGAAC

>RXA02507-upstream
ATTACCCACAATTCAATCGGTTTATACAACCAGCCTCTAACTGGCAACAGGACTGCAGA
CAGAACTGTTGCTGGAACCTTCGATGAACAGGATCGACA

>RXA02507
ATGAGCGAACAACCTTCAGGGTGTAACCTCACTCCGAATCAACTCCGGGCAAGACGCCCAAG
CGAGCAGCACTATCCAGCTGGATCGGCTCAGCTCTCGAATACTACGACTTCGCTGTTTAC
GGAACCGCTGCAGCGCTGGTTCTTAACCACCTCTTCTCCAGCTGATACTTCACCAAGC
ATCGCAATTTTGGCTGCGATGGGTACCGTGGGTGTTGCTTATGTGGTTCGCCCTCTGGT
GCGCTGATCATGGGTCCATTAGGTGACCGTTACGGACGTAAATTTGTCTCATGCTGTGC
CTCTTCTGATTGGAGCATCCACTTTTCGAGTTGGCTGCTTGCCAACATTTGATCAGGTC
GGTTACTTGGCTCCGGCACTGTTGGTGCTGTGCCGTGTGATCCAGGGACTGTCTGCATCC
GGTGAGCAGTCCAGTGCGATTTCGGTTTCTTGGAGCACGCCGATGAGCGTCACCGCGCA
TTTACTGTAGCTGGACTCTTCACGGAACCCAGTTCGGTACCTTGCTGGCAACCGGAGTA
TTTATCCCATTCACCTTGTTCTCTGAGTGAAGATGCTCTAATGTCATGGGGTTGGCGCGTT
CCGTTCTGGCTGTCCGCTGCTGTTGTTTGGTTGCTTTCCTCATCCGTGCTGGACTGGAA
GAGCCACCAGCATTCGTGAAAACAAGGAAGCAGTTGCAGGCGCAGCATCTCCACTGGCG
ATGACCTTGCGTTACCACAAGGCGCGGTTGCTCGCGTTGCTATTGCTGCGATGATCAAC
TCCGTGAACATTGTGTTTACTGTGTGGGCACTGTGTTCCGCCACCAACATTGTTGGCCTG
GATCGTTCAACTGTTTTGCTGGTTCCAGTTGTTGCGAACTTGGTTGCATGATTGCGATT
CCTTTGTCCGCGATGCTGGCTGACCGCATTGGTCCCGACCAAGTGTTCATCATGGGTGCC
ATTGTTGGTGGCTGGCCATGAACGGTTACCTGGGAGCTATCTACTCCGGCAATTGGACC
ATGATCTTCTTCATGGGCGTGTGATGTCTGGTCTGCTGTACTCCATGGGTAATGCCGTG
TGGCCAGCGTTCTACGCAGAAATGTTCCCAACCTCTGTGCGTGTACCGGCTTGGCTCTT
GGAACCTCAGATTGGTTTCGAGTCTCTGGTGGTTTCGTCCAGTTATCGCATCCGCGCTT
GCTGGTGATCAGGGTGACCAAGTGAAGGTGTCCATCTTCGTTGGTGTGTTTGTGTG
ATTTCTGCACTGGTTGCCATGACCGCTAAGGAAACCAAGGCTCTGACTCTGGATGAGATC
GATGCTCTGCACACTGCTGGTGGTGAGGCCGACAGCTGGCAGCCGCAAGCAAAGCCTCC
GAGGCCCAACTCGCGGCTCAG

>RXA02507-downstream
TAAAACCAAAAGGAATCTTTGAC

>RXA02515-upstream
GTGGCTAAGCACAGTTACTTGGCCAAGCTGGGCGGCAGAAAAACCGGCCAGCTAATACT
TCAGTTTAAATTCGCTTCAACCCGTGAAAGATTGTGACAG

>RXA02515
ATGAGCACTCTTGAAATCCGTAACCTGCACGCACAGGTCTGCCGTCCGATGAGTCCGCT
GAGCCTAAGGAAATCCTCAAGGGCGTCAACCTCACCATCAACTCTGGTGAGATCCACGCC
ATCATGGGCCCTAACGGTTCGGGCAAGTCCACTCTTGCTTACACCCCTGGTGACACCCA
CGCTACGAGGTAACCGCAGGCGAGGTCTCTCGACGGCGAGAACATCCTGGAGATGGAA
GTTGATGAGCGTGCACGCGCTGGTCTCTTCTGGCCATGCAGTATCCAACCTGAAATCCCT
GGCGTTTCCGTTGCTAACTTCCTGCGTTCCGCGAGCGACCGCAATCCGCGGCGAGGCTCCT
AAGCTTCGCGAGTGGGTTAAGGAAGTCCGCACCGCTCAGGAAGCTCTGGCAATTGACCCT
GAGTTCTCAACCGCTCAGTCAACGAAGGTTTCTCCGGTGGCGAGAAGAAGCGCCACGAG
GTTCTGCAGCTTGATCTGCTGAAGCCAAAGTTCCGCGATCATGGATGAGACCGACTCCGGC
CTTGACGTGGATGCACTGCGCATTGTTTCCGAGGGCATCAACTCCTACAAGCAGGAGACC
GAAGGTGGCATCTTGATGATACCCACTACAAGCGCATCCTCAACTACGTTAAGCCTGAC
TTCATTACGTTTTTCGCGAATGGCCAGATTGTGACCACCGGTGGCGCTGAGCTTGCTGAC
AAGCTCGAGGCTGACGGCTACGACCAGTTCATCAAG

>RXA02515-downstream
TAACATGTCCGATTTCTCAATG

>RXA02562-upstream
CGGGTGCCTGAGGGTGAGGTTGGGGCGACGAGGCGTGCATGGACTTTAGGTTAGGTTAT
TGAGCAGATTTATTTGGGCTTTTGTCTAGGGTGGGGAGCT

>RXA02562
ATGTTCTTGACAAAGGTTTCGCTGCTTGATCATCCGGAGTCATTGCCGGGGTATTTATCG
AGCCTGGCGATCGTGGAATATCTGCATGAACAGCCGTTGGAGTTTCGTGCACCGATTACT
GTGATTACTGGTGAAAATGGGGTGGGTAAATCCACGTTGGTTGAGGCTTTGGCGGTGGGG
ATGCGCCTTAATCCGTCTGGTGGCTCTAGGCATGCAAACCTTTGGCAGGGAAGGCGATATT
GTGTGCTGCTTCATCAGTCGTTGAAGTTGGTGCAGAGAGAAAACCTCGGGATGCGTTC
TTTTTTCGGGGTGAGACGATGTATAACGTGGCTTCCTATTATGAGGAGTTAATGGGGGAA
AAGAACATGCATGATCTTCACAAGATGAGCCATGGCGAATCGGTATTTGCGGTGATTGAT
CGGCGTTTTAACAATCAAGGATTTTTTGTGTTTGGACGAGCCTGAGGCAGGCCTTCCATG
CTGAGGCAGTTGGAGTTGTTGGGAAAGTTGGGCAACCTTGCTCGAGGTGGTGGCGAGATC
ATCATGGCTACGCACCTCTCCAATATTGTTGGCTATTCCGGGGGCGAGAGATCCTTGAAATT
ACATCTTCGGGTGTTGCAAAGGTGAATTTTGGAGATGCGGAGGCTGTTTCGTGCGGCTCGG
GAATTTGTGGCAGATCCGCGAGGTACGGCGGCGTTTCTGACTGCGGAGGAGGATCACCAA

>RXA02562-downstream
TGATGCCGTATATCACCGATATT

>RXA02595-upstream
GTGGGTAAAGGGGACTCCGAGGAAGTCCACGTCGTCTTCTTTTCGCGGCGCTGAGGATGGT
TTTCGCGGATTTGTGCGGGGGAGTGGGTGGGAGAGAAAACG

>RXA02595
GTGATCGTTGTGGCCATGGCTTCCATTATGGCTTGTTTAAAAGCAGCTAGACTGAATAAC
CCTATGAAGATCCTTTTGTGTGCTGGCGTGATACCACTCATCCTCAAGGTGGCGGAAGT
GAACGCTATCTGGAGCGGGTGGGTGAGTTTTTGGCGGATCAGGGCCATGAGGTGGTGT
CGTACTGCTGGGCACACGGATGCGCCACGGCGTTCTTTCCGCGATGGTGTGAGGTATTCC
AGGAGCGGTGGGAAGTTTAGTGTGTATCCCAAGGCGTGGGTGGCCATGATGTTGGGTGCT
GTGGGGATTGGCACGTTTTTCCAAGGTTGATGTGGTGGTGATACGCAGAATGGCATTCCG
TTTTTTGGAAAGTTTTTCTCCGTAAGCCGACTGTGTTGCTCACGCATCATTGCCATAAG
GAGCAGTGGCCGGTGGTGGGTGCGGTGCTGGCGAAGGTTGGTTGGCTGATTGAGAGCCAG
ATCGCGCCGCGCGCTTACAAAACCTGCGCCGATGTGACTGTTTCAGAGCCGAGCGCTGAG
GAGCTCATTGCGTTGGGTGTGGATCAGCAGCGGATTATATCGTGCGCAATGGCGTGGAT
CCCGTGCCGCTGCACACGCCGAAGCTGGATCGCGATGGCCAGCATGCGGTG

>RXA02597-upstream
ATACCCACTTTGCAAGAATTACAAACGGGGGCACCCTCAATGACTTGAAACACTTTATAG
AGTAGAAAGTGAGTCACGACACTTTTTAAAGGAGGATGCT

>RXA02597
TTGCCCCGAACAAGACTTAACCACCTTGGCCAATGATTGGCTCCAAGCTTTTGAAAAGGCC
ACTGCTAGTTCCAGCCCTGATGAAGCTGCCACTGCAGTCGTGCAACTTTTTGAGGATGAA
GGATACTGGCGAGACCTTCTTGCAATTCACGTGGAACCTCACCACCGCTGAAGGTGCAGAT
GAAATCGCCGAGATGATTGCAATACGTGGCCATCAAGCATCTTCCGAAACGTTGAGCTA
AAGGGCGAACCAGCTGATGAAGGAGATGGTGTCACTCGCGTACATTTCTCCTGCGAATCC
GCAGACTTCAAGTGCACGGGCATTGTCCGCCTTCGTAATGGCAAGGCGTGGACGCTACTC
ACCTCAGCTCGTGAGCTCCTGGAGCACCCAGAGCCCAAGGGGCGCAACCGTGAGATGGGC
GTCGTCCATGGACAAAATGAGGACACCCGAAATTGACTGACCGCAAGAATGATCGACAA
GCAGCGTTGGGTGTCACCGAGCAGCCATACACCCTCATCATCGGTGGTGGACAGGGTGGC
ATTGCTTTGGGCGCAGACTCAAGCGACTTGGTGTACCCGCTCTAATCATTGATAAAGCA
TCTCGCCCGGGCGACCAAGTGGCGTAGCCGTTACCATTCTCTGCTGCACGATCCAGTT
TGGTACGACCACCTGCCTTACATTCCATTCCCAGATCATTGGCCAGTATTTACTCCAAAG
GACAAGATGGGTGACTGGCTCGAGCACTATGTCCGCATCATGGATTTGGACTATTGGACC
AACACCGAGTGCCTGCGCGCCTCATACAATGAGGACACCAAGCAGTGGGATGTGACGGTC
AATCGTGATGGCGCGGAGTCCACGCTCCACCCACCCAACTAGTCATGGCTACTGGAATG

TCGGGCGAGCCCGAACAACCAACTTTGCCTGGCCAGGATAAGTTCCAGGGTGAAATTCCGG
CACTCTTCAGAGCACCCCGGCGGCGATGTCGATCGCGATAAGAACGTTGTAGTTCTGGGG
GCTAACAACTCAGCCACGACATCTGCGCGGATCTTTATTCCAATGGTGCAAAGCCCGTG
ATGATTACAGCGCTCGTCTACACACATCGTGCGTTCTGATTGCTGATGCGCGAAGTCTTC
GGGCTCTCTATTCTGAGGATGCCGTTGAAGCCGGAATTGATACCGATACTGCCGATCTC
CTGTTTTCGTCGTGGCCATATAAGGTGCTGCCAGGTGTGCAGAAGCAGGCTTTTCGACAAG
ATCCGTGAGGACGACAAGGAGTTCTACGACAAGCTTGAAAATGCTGGATTCTTGCTTGAT
TTCGGCGATGACGATTTCGGGGCTTTTCTTAAAGTACCTTCGCCGTGGCTCTGGCTACTAC
ATCGATGTGCGCGCCTCTGAAGTGGTGGCTGATGGAAGATTCCGGTGCGCTCCAATGTC
AGCATTGAAGACGTCAAGGAAAACCTCTGTGGTGCTCACAGATGGTACTGAGCTCCAGCT
GACGTGATTGTTCTAGCGACCGGCTATGGAACATGAACAACCTGGGTGCTCAGCTGGTT
GATCAGGAAACCGCTGACAAGGTGCGCCCATGCTGGGGTCTGGGCTCTGAAACCAACG
GATCCAGGCCCATGGGAAGGCGAGTTGCGCAATATGTGGAAGCCCAACACGTGGATTTCG
CTGTGGTTCCATGGTGGCAACCTTCACCAGTCACGCCATTACTCACGGTATTTGTCCATG
CAGTTGAAGGCGCGCTACGAAGGTATGAACACTCCGGTGACAGCAAG

>RXA02597-downstream
TAGATACAAAGAAAAGGGCATCT

>RXA02605-upstream
TCCGATCCTGTCTATCTACATGTGGGAGACTTTCCTTACCCAGGAATTGCCTGCATACCTT
GAGCAGAACTTCGGCGTTGCGCGAAACAACAACCTCCATTG

>RXA02605
GTGGCCTGTCCATGGGCGGGAACCTGCCGCGCTGAACCTCGCAGCAAAGCACCCAGATCAG
TTCCGCCAGGCTATGTCTTGGTCCGGCTACTTGAACACCACTGCGCCAGGCATGCAAACC
CTGCTGCGTGTGGCCATGCTGGACACCGGTGGATTCAACGTCAACGCAATGTATGGCTCA
ATCATTAAACCCACGTCGTTTTGAAAACGACCCATTCTGGAACATGGGCGGCTTGGCTAAC
ACCGACGTCTACATCTCTGCAGCTTCCGGCCTGTGGAGCCCTCAGGATGATGGAGTTCGC
GTAGACCACCGCCTCACTGGTTCTGTGCTTGAATTCGTGGCAATGACATCCACCAGGATT
TGGGAAGCAAAGGCAAGGCTTCAGGGTCTGAACCCAACCTGCGGATTACCCAATGTATGGC
ATTCACGGCTGGGCTCAGTTCAACTCCCAGCTGGAGAGAACTCAGGGTCGTGTTCTAGAC
GTCATGAACGCCTGG

>RXA02605-downstream
TAGAGCCACACCAAGGCCACAC

>RXA02614-upstream
TCATTGTATACGCCACCCTCGGTCTGCTGTCTGAAGCGCTGATCAGAGCTTGGGAACGTC
ACACCTTCGGCTACCGAAACGCATAAGAAAGTTGCTCGCC

>RXA02614
ATGACTGCCACATTGTCACTCAAACCCGAGCCACTGTCCGTGGATTGCGCAAATCATAC
GGAATAAAGAAGTCCTCCAAGGAATCGACCTCACCATCAACTGCGGCGAAGTAACCGCG
CTGATCGGACGCTCAGGTTGAGGAAAATCCACCATCCTGCGCGTGTGGCGGGCCTATCT
AAAGAGCATTCGGCTCTGTAGAAATTTCCGGAAACCCGGCCGTTGCCTTCCAAGAGCCT
CGCCTGTTGCCGTGGAAAACGGTGCTCGATAATGTGACCTTTGGCCTCAACCGCACTGAT
ATTTCTGGTTCAGAAGCACAGAAGCGCCCTCGGCACTGCTTGAGAAGTCAAACCTTCCC
GACTCCGACGCGCCTGGCCCTCACGCTCTCCGGCGGCAAGCCAGCGGCTCTCCCTT
GCGCGAGCGCTCATCTCCGAGCCAGAGCTTTTGCTTCTCGACGAACCTTTCGGCGCCCTC
GATGCTCTGACAAGACTGACAGCCCAAGACCTGCTGCTCAAAACCGTGAACACCCGAAAC
TTGGGAGTTCTGCTGGTCACCCATGATGTTTCCGAGGCCATCGCCCTGGCCGACCACGTC
CTTCTTCTTGACGACGGCGCCATCACACACAGTTTGAAGTGTAGATATCCCGGGCGATCGC
CGCACCCACCCCTCCTTTGCCTCCTACACCGCTCAACTCCTTGAGTGGCTCGAAATCACC
ACACCTGCC

>RXA02614-downstream
TAGAAAGAAATCATGAAATTTAA

>RXA02616-upstream
AGTGTTACTTCCGGTAGATAACAAGATGGTCTCAATTAACTTCGATAGCGTGATATAAG

CTTCGAAAAGTTTTGTGGCAAGAATCGGAAGCAGGCGAAA

>RXA02616

TTGCAGAAGCACACTCGAGGTGGCAAGCACCGCAAGCAGACTACCTCCCCAGTAACTAAG
GGTGGTGTGCTTTTTGTTCAGTAGCTACCGGTGCCGTGTCAACTGCAGGCGCAGGCGGA
GCAGTTGCTGCACAGGCTTCCAATCAGCCCGTTGAGGTCAACTTCGAGCTTACTGCAAAC
GACACAACAGACCTCGTGGCTGGAAGCTCCGCCCCCTCAGATCCTGTCCATCGCTGAGTTC
AAGCCAGTTGTGAACCTGGGCGATCAGATCGTTAAGACCATTAGTACAACGCTGACCGC
ATTCAGGCTGACCTGGACGCTCGTGGCCCTTCAGTGGTTCGCCCTGCTGAAGGTTCTTAC
ACCTCCGGCTTCGGTGCTCGTTGGGGCACCAACCACAACGGTGTGGATATCGCTAACGCA
ATCGGCACCTCCAATCCTCGTGCCATGGACGGCACTGTTATCGATGCAGGTCTGTCTCC
GGTTTCGGTAACTGGGTTCCGCTCCAGCACGAAGATGGCACCATCACCGTGTACGGCCAC
ATGGAAACCGTTGAGGTGACCGTTGGTCAGACTGTTAAGGCTGGCGAGCGCATCGCAGGC
ATGGGTAGCCGAGGATTCTCCACCGGCTCCACCTCCACTTCGAGGTTTACCCTGCAGGC
GGTGGCGCTGTTGATCCAGCTCCTTGGCTTGACAGAGCGCGGCATTACTCTT

>RXA02616-downstream

TAATTAACTTTTGGGCGACCCTT

>RXA02627

GATGTCACCTGTGGAAAGCCAACCAGAACGCGTCGTTGCCCTGGGTTGGGGAGATGCTGAG
GCTGCGCTGGAATTCGGTGTGCAGCCTGTGGGTGCATCAGATTGGCTCGCATTCGGTGGT
GAAGGCGTGGGACCGTGGATTGAGGATTCTGCCTACGATGAAGCGCCAGAAATAATCGGA
ACCATGGAACCGGAGTATGAAAAGATTGCAGCGCTTGAACCGGATCTGATTTTGGACGTG
CGCAGCTCTGGCGACCAGGAACGCTATGACAAGTTGTCTTCAATCGCACTGACCATCGGC
GTTCCAGAAAGGTGGCGATAGCTACCTCACCCACGCGCTGAGCAGGTAACCATGATCGCC
ACTGCTCTGGGGCAGGCTGAACGTGGTGAAGAAGTGAACGCTGAATACGAGCAGCTCACT
GCTGATATTCGTGCAGCTCACCCGGGCTGGCCTGAGAAGACCGCGGCTGCTGTATCTGCA
ACGGCAACCAGCTGGGGTGCATACATCAAGGGCTCCAACCGTGTAGATACTTTGCTGGAC
CTGGGCTTCCAGGAAAACCTGAGCTGGCTAAACAGCAACCTGGCGATACGGGTTTCTCC
ATCAAAATTCAGTGAAGAGACTTTCGGCGTTGTGGATTCCGACCTGGTTGTGGGCTTTGCC
ATCGGTATGACTCCTGAGGAAATGGCAGAGCAGGTTCCATGGCAGATGTTGACCGCCACT
CGTGACGGCGTTCCCTTTGTGATGCCCCGTGAGATTTCCAATGCGTTTTCTTTGGGTTCC
CCGCACTCCACTCGGTTGCGGTTAGACGCCTTGGTGCCACTTCTGGAGGAGCATGCAGGG
GAG

>RXA02627-downstream

TAGTGGTCCGGTGGTGCGGGCAG

>RXA02628

ATGCTTGAAGGTTTTAGAGATTTCTGTCCTTCGGGGAAATGTCATTGAACTCGCAGTTGCC
GTGGTCATCGGTACTGCCTTCACCGCTATCGTGACAGCATTCTCCGAGAGCATCATCAAC
CCATTGATCGCTTCCATCGGCAGCACAGAGGTTGAAGGCTTCGGCTTCCACATCCGCGCC
GGCAATGCCGCAACATTCTGTGGATTTTGGTGCTGTCATACCCGAGCGATCAACTTCCTC
ATCATCGCAGCAATTGTCTACTTCTGTTCTCGTTGCTCCAATGAACAAGCTCAGCGAAACC
CTCGCAAAGCGCAAGGGTGTGAAGAAGACGAGACCCAGCTTCCATCGAAGCAGAACTC
CTCACCGAGATCCGCGATCTCCTGCAGGAGCAAAAGCGCCTTCAG

>RXA02628-downstream

TAGTTAAAAGGCCCTAAAAGCAC

>RXA02650-upstream

GAATTTTTGCTGCAACTGTGTAAAAACCAGCGCTGAATTAAAGATCACCTTTCACCCTTA
ATTGAGCCTGGGTGGAAGTTTCTACCGCTCATGGGGAAAG

>RXA02650

ATGGTCAACGTGACCTCAAAGGATGCAGGGGCAAACGTGACCCCCATGAGTAAGAAAGAA
AAGAGGACAACCGTTAAACAGGTGGTTGCCTTGATGGCCGCCATCGTTGTGGTGATTGCG
TCCCTAGACCAAATAGTCAAGCAGATTATGCTTAGTTGGTTGGAACCTGGCGTTCCCGTT
CCCATCATTTGGGGATTGGTTCCGCTTCTACCTCCTGTTTAACCCCGAGCCGCATTTTCG
ATGGGTGGGGAACAGCACCTGGATCTTTACAACCATCCAGTTGAGCTTCGTATCGGT

ATCGCAATTTATGCCCCACGCATCAAACACAAGTGGATCGCGGCAGGACTTGCCCTTGTT
GCCGGTGGAGCCTTGGGAAACGTGTGGACCGGTTGTTTCAGAGATCCTTCCTTCTTCTTC
GGACATGTTGTTGATTACATCTCCGTAGGAAACTTTGCAGTATTTAATATCGCCGATGCC
TCGATTTCTTGCGGCGTCTGTTGTTTCTGATCGGAATGTTCTTGAGGACCGTGAAAC
CCCCAGCATGCCAAAGCAACTGACGAGAAGGATGAGGCC

>RXA02650-downstream
TGATGAACAACCGACAAAGCAGA

>RXA02660-upstream
CATTTTTTCAGCACACTTTTTAAGATCTCATCGAAAGCGCGATACCCACTATGTCCAATCT
TTTGAGACTTGTTCGGCCGACGGCTCATCGCTTTACCGATC

>RXA02660
ATGATTATTGGCGTCACCCTGCTGGTTTTTCATCGTCATGTCATTCTCTCCTGCCGACCCG
GCACGACTTGCCCTAGGCGAATCAGCCTCCCCGAAGCACTTGAAGCCTACCGTGAAGCC
AACGGCCTCAACGATCCAATGATGGTTTCGCTATTTTCTGACTTCATCCTCGGCATGCTCAA
GGCGACTTGGGAACCTCTAGCGGTGGCGTAGCTGTTACCGACATTGTTGCCCGCGCTTTC
CCCATCACCCCTGCAGCTAACATTTCTGGGGACTCATCATCGCTGTTGTAGTGGCGTTGATC
CTCGGTGTCATCGCCGCTCTATACCGAGACCGCTGGCCTGACCAGTTGATTCGCGTGGTC
TCCATTGCGGCTCTTGTACTCCTTCATTCTGGTTGGCTATCTTGCTGATCCAGTGGTTG
GGTACTATCCCTGGAGCCTGGGGTTTCTTCCCAGCACTTGTCACCCGGTGGGTCCCATTC
AGCGAAGATCCCGCCACCTACTTCAACAACATCGCACTTCAGCGATTGCGTTGGCAGTCC
CCGTTGCAGGTTCTTTGGCCCCGCTTGTTCGTACCTCCATGGTGGAAGAACTGGACAAGG
ACTACGTCGCGACAGCAATCGGTGCAGGATCCCCAAAAC

>RXA02660-downstream
TGAAGTTGTTGCCCGCAATGTTT

>RXA02661-upstream
TGGACAAGGACTACGTCCGCACAGCAATCGGTGCAGGATCCCCAAAACCTGAAGTTGTTGC
CCGCAATGTTCTGCGCAATGCGCTGATCACCCCAATCACC

>RXA02661
GTGATTGGTCTTTCGCGTTGGTTCCCTCATGGGTGGTGCGGTGATCATTGAGATCATCTTC
AACATCCAAGCAATGGGACAGCTCATCCTAGACGGTGTGACCCGAAATGACGTCTACCTC
GTCCAAGGTGTCAACCTCACCGTTGCCATCGCCTTCATCATCGTCAATATCGCCGTGGAC
CTGCTCTACGTCTTGGTCAATCCACGTATTAGGAGCATC

>RXA02661-downstream
TAGATGCGCCGTAAACTAACCAC

>RXA02663-upstream
GTGCAAAATATCTGTCCAGTTCGTGAGACTACGTCAATGCTTCCAAGGTCATTGGCGCATC
AACCGCTCACATCTTGATCAAGCACGTTGCCCGAAACTGC

>RXA02663
ATGGCTCCGATTCTGGTGTTCGCCACCGTCTGGTGCCTGATGCGATTGTCTTCGAAGCA
TCCCTGTCTTCATCAACGCTGGTGTGAAACCACCATCACCTTCATGGGGCAACATCCTT
GCCGATGGTAAAGCCCTGCTGCTTAGCGGCGCATGGTGGCCAACCTTCTTCCCAGGTTTG
ATGATCCTGCTGACCGTTCTCTGCTTGAACATCCTTTCTGAAGGCCTCACCGACACCCCTG
GCCAGCCCTAAGCCAAAGCCTGTTTCAGCTTCTGCAAAGAAGGCACTGAAGAAGGAAGAA
TCCGGTGAAAAGGAAGGCTCCGGAATCGTGCTTGGGCACACCACACGTGAAGAAGCCAAC
GCCTCACTGCTCGCATCACTTGCTGCGCTATCCACCAGCGAAAACAATTCCAATAACCGG
CTTATATTTGATGGCAACCCCACTCCTCTGTTGGAAGTTCGCGATCTAAAGATCTCCTTC
CCCAATGCTCACGGAGATATCAATATTGTCGACGGCGTGAACCTCACCGTCGCCCCAGGC
CAACCATGGGTCTTGTGCGTGAATCCGGCTGTGGTAAATCGATTACCGCAATGTCGATC
ATGGGTCTGCTGCCCTCCAACAGCAAAGATCGAAGGCGAGATCCTTTTCGACGGAAGAAC
CTCCTTGATCTGAAACCAGACGAGCTCAATGCACTGCGTGGACATGAAATCGCCATGATC
TACCAAGATGCACTCTCCTCACTCAACCCATCCATGCTGATCAGCGCCCAATGAAGCAG
CTGACCCGCCGCGGTGGAAAGCGCAGTGCCGAAGAACTCCTGGAACCTGTAGGCCTTGAT

CCAAAGCGCACCCCTGCAGTCCTACCCGCATGAGCTTTCAGGTGGCCAGCGCCAGCGAGTT
 CTCATCGCAATGGCACTGACCAGAAACCCACGCCTCCTCATCGCCGACGAGCCAACCACC
 GCGCTAGACGTCACTGTTTCAGCAGCAGGTTGTGATCTGCTTAATGAACTGCGTGAAAAG
 CTCGGATTTCGCCATGATCTTTGTATCCACGACTTGGCTCTTGTGCGCCCGCTTGGTGCAC
 AAGCTCACCGTCATGTACGCAGGTCAAGTTGTTGAGCAAGGAACACCCGCGAAATCCTT
 ATCGATCCTCGACACGAATACACCCGCGGTTTGTCTCGGATCCGTGCTCTCCATCGAAGCT
 GGTGTGGACCGCCTCTACCAGGTCCAGGCACGTGTTCCATCACCAAAGGAATTCGTGGCA
 GGCGACCGCTTTGCACCACGATCAGAATTCACAGAACTTGGCCTTGACCAAAGCCAGTA
 CTTGCGCCCATCACGGGCACAGAGCATGCATACGCAGCAACCGATGAACCTTCTTGCCGCA
 AAGGGAGAACAACGA

>RXA02663-downstream
 TGACCTCGACAATCGACACCAGG

>RXA02664-upstream
 ATCCACAAAGACCCGTACCGGAAAGCTGTTTCGCCCAGACCAGGTCCACGCCAACAAAA
 CATCAACTTCAAGGCCTACCGCGATGAAGTAATCGGCATC

>RXA02664
 GTGGGTGAATCTGGTTGCGGAAAATCTACCCTTGCCCGCGTTATGGTTGGCCTGCAACCG
 GTCACCTCCGGCGAAGTGCTGTTCAAAGGCAAGCCCATGAAGCCTCGTGGTGCGCAGCGC
 AAAGAACTCGGCAGCTCAGTATCCGTGCTGTTCCAGGATCCTGCCACCTCGTTAAACCCA
 CGAATGACCGTGCGCGAACAGCTCCTCGATCCACTTCGAGTACACAAAGTTGGCGATGAA
 GCATCCCGCAACCACTGGGTTTCAGAGCTGATCTCCATGGTTGGCCTCCCGCAATCCGCG
 TTGGAAGTACTCCCCCGACAGGTTTCCGGTGGCCAACGCCAACGCGTGGCCATTGCTCGA
 GCACTTGCGCTGAAACCTGACATCATCGTTGCCGACGAACCAACCTCCGCGCTGGATGTA
 TCCGTTCTGCGCAGGTCTCAACCTTCTGCTGGATCTGAAAACCTGAACTCGGCCTGGGA
 TTGGTATTCTATCTCCACGACATCAACACTGTTGCTACGTTTCTGATCGCATCGCAGTC
 ATGCTGGCTGGAGAAATCATTTAGGAAAACACCACCTCAGAGATCTTCAACAATGCGCAG
 CAGGACTACACCCGCACTCTGCTCGAAGCGACACCATCGCTGCTGAACAAAACCTCGTTTG

>RXA02664-downstream
 TAGTCTCCAACCCCTTTATTCCTT

>RXA02684-upstream
 GCAGGTTCGTCCACAGCCGCGGTGATTGCAGGGGATGGGGGGAGGCGTCGAAAAGCAAT
 ATCTTTTAAGCCCCGTGGCTGCCTGGGCACGATCGCGGGC

>RXA02684
 GTGCTTGCTGTGGGCTTGGTGCTTGTGTTTGTGGTGACGCTGTGGGCGGATTCTGAAGCTG
 AATCGCGTGGATGCCACGCCTGCGACGCAAGGTGGCGAACACTGCCGGAACGAACCTGGCTG
 CTGGTAGGTTTCGATTTCGCGGCAGGGTTTAAGTGATGAGGATATTGAGCGGCTAGGTACC
 GGCGGCGATATCGGTGTGGGCGGTACGGACACGATCATGGTGTGTCATATGCCGCGTACT
 GGCGAGCCGACGCTGTTGTGATTTCCGCGTGATTCTTATGTCAATGTCCCTGGCTGGGGC
 ATGGATAAGGCAAACGCCGATTTACCGTGGGTGGCCCGAACTGCTGACGCAAACCGTG
 GAGGAGGCAACTGGCCTGCGAATTGATCACTATGCAGAAATCGGCATGGGTGGTTTGGCG
 AACATGGTTGATGCCGTGGGCGGCGTGGAATGTGTCCTGCTGAGCCGATGTATGATCCG
 CTCGCGAACCTGGATATTACGGCTGGTTGCCAGGAATTTGATGGGGCAGCCGCGTGGGT
 TATGTGCGCACTCGTGCCACAGCCCTGGGTGATCTGGACCGGGTGGTGCGTCAGCGGGAA
 TTCTTCTCCGCTCTGCTGAGTACAGCTACGTCCCCGGGCACGTTGCTGAATCCGTTCCGC
 ACCTTCCCGATGATCTCCAACGCGGTGGGAACATTACCGTTCGGCGAGGGCGATCACGTG
 TGGCACCTGGCCCGATTGGCGCTGGCGATGCGCGGAGGAATCGTGACGGAGACCGTGCCG
 ATTGCCTCATTCGCAGATTACGATGTGGGAAATGTTGCGATTTGGGACGAAGCTGGAGCC
 GAAGCACTATTTAGCTCCATGCGC

>RXA02684-downstream
 TAAAACCCAGGTAATCGTTTAC

>RXA02728-upstream
 ATCCCATACGTTGCCTTCCGATCGGCATTTTTCACAGCGCTGGTTCGGCGGCCAACATTCT
 TCATAATGTTGCGCCGAATGATGAAAAGGGCGTGCACTAA

>RXA02728

ATGGCCATTGTTTTCCCTCGACAACGTCACCGTATCCATTGAAGGAAAAAAGCTTCTCGAC
GCCGTCTCCCTCAAGGCCTACCCCGGGGAAGTGTGGGACTCATCGGCCCAAACGGTGCC
GGAAATCCACTCTGCTGAGTGTCTTTTCAGGCGATCGGCTTCCCGATTTCAGGCGAAGTC
AACGTCGGTGGCTTAGATCCCGCAACAGCAGCGGCATCCGATATGGCCAGGGTGCAGCA
GTCATGCTTCAAGATGTCAGCGTGGCATTTCCTTCCTCGTGTGGGACGTCGTAGAAATG
GGCAGGCGGCGCTGGCAGAAGGCGTCAACCCCGAAGAGGATCATGAAATCATCGAAGCA
GCGCTTGGCGCCACCTCGGTATCGCACCTTGCCGAACGTGAAATCACCACACTGTCAGGC
GGCGAGCGGGCACGCGTTGCCTTGTCCCGTGTCTTGTCTCAGCAAACCCCATTTGTGCTG
TTGGACGAACCAACAGCCGCGATGGATATCAGCCACCAAGAACAACTCTGGGCACAGCG
CGAGCACTGGCAGCCGCGGGGAGCAGTGATTGTGGTCTTCATGATCTCAATGCGGCC
GCTGCATATTGCGACAGCATTGTGTGTCTCAGTGATGGTCGAGTGATTGCCTCCGGTTCT
GTTGATCAGGTGATTCCACGGAAACGCTGTCCCGTGTTCACGGTTGGCCTATCAGGGTC
GATCATAGTGGAAATATGTTTCGAGTGGAGCCGACCGTTCTGAGGCGAATTTACCCTCC
GTACTACAGGTGAAAAATACGGTTTTACCAGCT

>RXA02728-downstream

TAGATACATGACTAATAAGGTT

>RXA02750-upstream

GTTCCATGGACGATGTATTTCTAGCAGTTACAGCTGAACGGAAACGATCATGATTACAGT
TCTGACACGCAGACACTTGCCTGCTTTTTCCGCGACCGC

>RXA02750

ATGGCAGTGCTGTTTTCCATCATGGGTGCGCTCATCCTTTTGGTCCTGTACGTGCTGTTT
TTAGGAAACTGCAAATTGACGGTCTCATGGTGGATCTACCTGACTCAGCCCGAGACGAT
GTTGAAGGATTTCGCTTCAATTGGGTGTTTTCCGGAATTCTCATCACGTCCGCAATCACT
GTTCCGCAAGCAGCACTTGGAGTGTGGTTGAAGATCGCACCCCGGAGGCATCAAAGAT
TTCCTCGTGGCACCCGATCCAGAACGACGCTGACGGTGTCTATATCTTCGCAGCAGTC
ATTGTCGCCATGACGATTTTGATCTTTGAAATCGTGGTGGGAAGTATTGGTTTAGCTATT
TTGGGGCACTTCAGCATGAGCATTGCTCGCGTGCTCGAATTGGTAGTCGCTTGTCTCTG
CTCACCTGGTGTTTTCCGCAATTGCAGCATTCTGATCACCTTGGTGAAATCTCAAGGC
GGAATGTCTGCGCTTTCAAGCCTGGTAGGCACCCTGGCGGGCTTTTTATCTGCTGCTTAT
ATTCCACCCATCGCATTGCCTGAAGCAGTGACAAACGTGTTGAACTTCTCCCGTTTACC
CCAGCTGGAATGTTGATCAGACAAATTGTGGTTGCCCCAGCATTGGACGCGATTTCACCT
CCACCCGAAGCCTTCGATATCTTCCAATTCCGATACGGACTCAAACCTGGAAATGTTTGGG
GAACCCGTTTCTACATGGGTGGCAGTAGGAATTGTTGCCTCATGGGGAGTGGTGTGGA
CTCATTGCCGCGTTCAAATGAAAAGCGTGGTGCGA

>RXA02750-downstream

TAAATCCTGCTAAAGAATGCTTC

>RXA02761-upstream

CAGGTTGTTCTCATTGAGGTGGTTTTCTCCGAGAATGCAGCTTTGATCGCCAACGTGGCGC
CAGAAGTGATCGCAGTTGTCGGGCATTTCATCGCACTGTGG

>RXA02761

ATGATGGATGGTATCAACCGCCGTACCACCCTCATTACCGGTTATTCTCTCACCACCATT
AGCCACGTATTGATCGGTATCGCATCCGTAGCATTCAGTCGGCGATCCTCTTCGCCCC
TACGTTATCTTGACTCTGGTTGTGGTCTTCGTGGGATCCATGCAGACCTTCCTCAACGGT
AGCTACCTGGGTTATGCTCTC

>RXA02761-downstream

TGAGCTCTTCCCGCTGGCAATGC

>RXA02762-upstream

TTCCAGTCGGCGATCCTCTTCGCCCCCTACGTTATCTTGACTCTGGTTGTGGTCTTCGTG
GGATCCATGCAGACCTTCCTCAACGGTAGCTACCTGGGTT

>RXA02762

ATGCTCTCTGAGCTCTTCCCGCTGGCAATGCGCGGTTTCGCAATCGGTATCTCAGTGTTCT
 TTCTCTGGATCGCAAACGCGTTCTCGGATTGTTCTTCCCAACCATCATGGAAGCAGTA
 GGACTAACCGGAACCTTCTTCATGTTTCGCCGGAATCGGTGTGGTTGCCTTGATCTTCATC
 TACACCCAGGTTCTTGAAGTCTGTTGACGTACCTTGGAGGAGATTGATGAGGATGTTACT
 TCCGGTGTCAATTTCAACAAGGACATCCGAAAAGGAAAGGTGCAC

>RXA02762-downstream
 TAAAAACCCAGACACTGCATAGA

>RXA02769
 ACAGTAGTTCCGGTGTACCTCGCTGAACTCGCACCACTAGAAATCCGCGGCTCCCTGACC
 GGCCGAAACGAGCTTGCTATCGTACCGGCCAGCTGCTTGCCTTCGTGATCAACGCGCTT
 ATCGCCGTCACCCCTACACGGAGTTATTGATGGAATCTGGCGCATCATGTTCCCGCTCTGT
 GCCCTCCCTGCCGTGCGCCTCTTCTCGGCATGCTGCGGATGCCGGAATCACCACGCTGG
 CTGGTCAACCAGGGGCGTTACGACGACGCCCGCGCGTTCATGGAGACCGTCCGTACCCCT
 GAGCGTGCGAAAGCCGAAATGGATGAAATCATCGCGGTGCACCTTGAAAACAATGCGGCA
 CTTCTCTGGTGTAAAGCAGTCTTCGGGCCAGGCTTCAGGCCAGGTTTCTAGCAAGCACACC
 CACATGTCCATCGCGCAAGTCTCAGCAACAATGGCTGGTTTCGTCTGCTCATCGCCGGC
 ATCGGTGTTGCAGTTGCCAGCAGCTACCGGCATCAACGCCATCATGTACTACGGAACC
 CGCGTCTCGAGGAATCCGGCATGAGCGCAGAAATGGCTGTGGTTGCCAACATTGCTTTC
 GGTGCCGTGCGGTTCATCGGTGGACTGATCGCACTGCGCAACATGGACCGCCTGGATCGC
 CGCACCACTTCATCATCGGCCTGTCACTGACCACCACCTTCCACCTTTTG

>RXA02795
 ATCGACGTCTCCCTCCCCGAACGCACCGCTTCGGCCTACCCACACGAACTTTCAGGCGGG
 CAACGCCAACGCGCACTAATCGCAATGGCGCTGGCCAATGATCCTGACCTGTTGATCTGC
 GATGAACCCACCACGGCTTTGGATGTGGTTGTGCAAAAACAAATCGTCGATCTGCTGCTG
 CGTCTACCAAAGAACGTGGCACCGCTTTATTGTTTCATCACCCACGATCTTGGACTCATC
 GCGCGCACCTGCGAACGCTTATTGGTGATGAAATCCGGCGAAACCGTAGAACGCGCGGAC
 ACCGAGGCAATTCTTCGCTCCCCCGCCCATTCGTATACCCAACAGCTCCTTGATGCTTCA
 ATCCTTGACCAGCCAGAAATCGCCTCAGATTCTGGCGCGCCGGTAGTGATTGATGTGGAG
 GAGGCGTCGAAAAGCTTTAAAGAAACCACGCCCTCCACAAGGTTTTCATTGGCGGTGCGC
 AAAGGTGACCTGCTTGGAAATAGTCGGCGGATCAGGTTCCGGCAAAACGACTCTGCTGAAG
 CTCATCGCCGGTTTGGATAAGCCCAACCGGTACCGTTGCGGTAACCGGTGGTGTGCAG
 ATGGTGTTTCAGGATCCCCAATCAAGCCTCAACCCACGGATGAAAATCAAAGACATTGTC
 GCCGAACCACTGCTTGGTTGGAACGCGGCGGAGAAAACACACGGGTTGCGGAAGTCATC
 ACCCAAGTGGGACTGAGCCCCGATGTCTTAGATCGCTACCCCAACGAATTCTCCGGAGGA
 CAGCGCCAACGAATCTCCATCGCCAGAGCCCTCGCCATCAAACCAGCGATCCTGCTTGCC
 GACGAACCTGTCTCCGCCCTCGATGTGTCCGTACGTAAACAAGTACTGGATCTTCTCCAA
 CAACTCGTCGAAGAATACGGCATCACCTTGGTGTTCGTCTCCACGATCTGGCAGTGGTG
 AGACACCTGTGCACAACCGTGTGGGTGATGGAACAGGGACGAGTCTTGAGCAAGGGCCC
 ATCGATTGCGTTTATGATCACCCACAGACCGAATACACCAAGGAGCTGCTTGATGCCGTT
 CCGCGGTTGAGCCTT

>RXA02795-downstream
 TAAACCAGCGCAGATGACAACGC

>RXA02808
 TTTTACTTCGGCATCCTCCAGTCCTTGCAAGAGTGCTTCCCACTTCGGCATCGAGCCT
 GTGGAAATGGCCCGCGCATCCATCACTGGCCAGCCCGTTACATGCAAAGCCCGCTGGTC
 CCAGCGATCCTCCTGCTGGTTTCCCTCGCCAACGTCAACCTTGGCGACCACCACAAGAAG
 GTTCTGTGGCGCGCCTGCATCGTGTCCATCGCGATGCTCGCCGTAGCCCTCTTCATCGGC
 GTCGTGCCACTCAGCGCA

>RXA02808-downstream
 TAAAATAGCTTTTCGACGCCAAA

>RXA02863-upstream
 ACGGACTGCCCATTGCGGTGCGCGATGATCCCGAAACCAGCTCACTTCGCGTGATCCCGC
 ATCCAAATCCCTTTTGATTGAAAGTTTGACTTAAAAACCC

>RXA02863
 ATGAAAAAATCACTCATCGCCATTGTTGCCAGTGCGCTCGTGTTAAGCGGCTGCACCTCT
 GATTCTTCTGACTCTTCCGGCACTTCCGGAACGTGTGGAAACCACTTCGATTACAACCAGC
 GTTGCCCGCAGCTGACGGCGCATTCACACGCACCGTCACTCGACGATTCCCTCCATCACC
 TTAGAATCCAAACCAGAGCGCATCGCCGTACTACCCAGAGGCAGCATCCTTGTTCTC
 CCCATCACAGGCGCGGACCGCGTCGTGATGACCGCCGAAATGGACACCGCTGACGAAGAA
 ACCGCAGCTCTGGCCTCCCAAGTGGAAATACCAAGTCAAAAACGGTGGCAGCCTCGACCCC
 GAACAAGTTGTGCGCGGCGACCCAGATTTGGTGATCGTCAGTGCGCGTTTCGATACCGAA
 CAAGGCACCATCGACATTTTGAAGGCCTCAACGTCCCCGTAGTTAACTTCGATTAGAC
 GCTTGGGGAGACATCGACGCCATCACCAAACACCTAGAAATTGTGGGTGAACCTCGTCGGC
 GAAGAAGACAAAGCCGCAGAAGCAATCGCAGAAATCGATGCAAACCGCATCGACATCGAC
 AAGCCTGCCACCTCCCCCACTGTGCTCACTTTGATGCAACGCGGACCACGCCAAATGGTC
 ATGCCAGAATCTGCCATGCTCAACGGCCTGATCCGCGAAGCCGGCGGCACTCCAGTGGTA
 GATTCTCTCGGCGCGGTAGGCACCATCACTGCAGACCCAGAACAAGTTGTTGCGATGGCA
 CCTGAGATCATCATTCAGGACTTCCAAGGTAAAGGCCGAGAGAACTTCGCTAATTTTC
 CTCTCCAACCCAGCGCTAGCCAACGTTCCCGCCATTGAAAACGACAAGATTTTCTACGCC
 GACACTGTCAACCACTGGAGTTACTGCAGGTACCGATATCAACCACTGGTCTGCAGCAAGTG
 GCAGAAATGCTGAGC

>RXA02863-downstream
 TAGTTTTGAGATGTTGAACTAG

>RXA02864-upstream
 CTTGCAAACAGGCGTGGTGGTGGCGTTTATTGGCTCACCAATTTTCCTTTATTTACTGCT
 CAGCATGCGCAAGCGACGCGGATTGGGGCTGTAAAACTC

>RXA02864
 ATGCCTCAATTAGTTGAAATTCGTGATCTCAACGTTGAATTCCCCTCTCGCCATGCAGTG
 AAAACGTTGCTTTTTTCTGCACCTGCTGGAAAAGTCACCGCACTGATTGGCCCAAATGGT
 GCTGGTAAAAGTACTGCCCTTTCGGCGATTGCAGGATTGGTTGAATCCACCGGCGAGGTA
 ATGGTTGGTGGGAGTGGGGTTGCGTCGAAAAGCGCTAAAGCCCCGAGCCCCGCTGCTCTCA
 CTCGTGCCGCAAAACACCGAGTTGCGCATTTGGTTTTAGTGACGCGACGTTGTGCGGATG
 GGCGCTACCCGCATCGTGGCCGTTTCGCCGTGGAGACCGACGAGATCGACGCGCCACC
 GATGACGCCCTGCGCGCCATCAACGCGCTCGACATCGCCGAGCAGCCGTTCAACGAATTA
 TCGGGCGGCCAGCAGCAGCTCATCCACATCGGCCGAGCGCTCGCCCAAGACACCGCCGTC
 GTGCTTCTCGACGAGCCCGTCTCCGCCCTTGATCTACGGCACCAAGTTGAAGTCCCTTCAA
 CTCCTGCGCGCCGAGCTAATTCGGCACCAACCGTGATCGTCTGCTTACGATCTCAAC
 CACGTTGCGCGTTGGTGGCAGCATGCAGTGTTGATGGCCGACGGCGAAGTTGTCTCCCAA
 GGTGACATCCGCGAGGTGCTCGAACCTGCCACACTGTCCACCGTGACGGACTGCCCAT
 GCGGTGCGCGATGATCCCGAAACCAGCTCACTTCGCGTGATCCCGCATCCAAATCCCCTT

>RXA02864-downstream
 TGATTGAAAGTTTGACTTAAAAA

>RXN00001-upstream
 TGTCAATAGGCAGCACTCTAGATGGCGCACAGTGACTCACTTCACTGTTTCTCACACTACG
 GATCGTTGCGCACGTACCTGCCGATGGAGGAGATTCTGCA

>RXN00001
 ATGGCAACCGTAACGTTCAAAGATGCTTCCCTAAGCTACCCGGGAGCAAAGGAACCCACC
 GTCAAGAAATTCACCTGGAAATCGCCGATGGCGAGTTCTCGTCTCGTCGGCCCTTCC
 GGCTGTGGTAAATCCACCACGCTGCGCATGCTGGCCGGTTTGGAAAACGTTACTGACGGT
 GCCATTTTTCATCGGAGACAAGGACGTTACCCACGTTGCACCGCGTGACCGTGACATCGCC
 ATGGTTTTCCAGAACTATGCTCTTACCCCCACATGACCGTGGGCGAGAACATGGGCTTC
 GCACTGAAGATCGCCGGCAAGTCCCAAGACGAGATCAATAAGCGCGTCGACGAAGCCGCC
 GCCACTTTGGGCCTGACCGAATTCCTGGAGCGCAAGCCGAAGGCCCTGTCCGTTGGTCAG
 CGTCAGCGTGTGGCCATGGGCGCGCCATTGTTGCAACCCGCAAGGTCTTTCTCATGGAT
 GAGCCGCTGTCTAACCTCGATGCCAAGCTGCGTGTTTACAGACCCGTACCCAGATTGCAGCC
 CTGCAGCGCAAGCTTGGGGTTACCACCGTTTACGTACCCACGACCGAGACGGAGGCTTG
 ACCATGGGTGACCGCATCGCGGTGCTGAAGGATGGCTACCTGCAGCAGGTTGGCGCGCC
 CGAGAGCTTTATGACCGCCCCGCCAACGTCCTTCGTGCGCGGCTTCATCGGCTCCCCAGCC

ATGAACTTGGGCACCTTCTCGGTCAAGGATGGTGACGCTACCTCTGGTCACGCTCGCATC
AAGCTTTCCCGGAAACCTCGCCGCCATGACGCCGGAGGATAATGGCCGCATCACCATT
GGTTTCCGCCCCGAGGCACTGGAGATCATTCCGGAAGGCGAGTCCACCGATCTTTCCATC
CCAATCAAGCTCGACTTCGTGGAGGAACCTCGGTTCCGATTCTTCTCTACGGCAAGCTG
GTAGGCGAGGGCGACCTTGATCCTCCAGCGAGGATGTCCCCGAGTCCGGCCAAATCGTC
GTCCGCGCTGCTCCGAACGCCGCGCCTGCTCCGGGCAGTGTTTTCCACGCACGCATCGTG
GAGGGCGGCCAGCACAACTTCTCGGCGTCGACTGGCAAGCGCCTCCCT

>RXN00001-downstream
TAAGCCCGCGTACCGGCTACCCC

>RXN00099-upstream
CTCTGGTGAAGAGGATGTTGACTCGGGAGATTCTTCCACTGATTCACTGATTAAGTGGTA
CCGCGCAAATAGGTAGTCGCTTGCTTATAGGGTCAGGGGC

>RXN00099
GTGAAGAATCCTCGCCTCATAGCACTGGCCGCTATCATCCTGACCTCGTTCAATCTGCCGA
ACAGCTATTACTGCTTTAGCTCCGCTGGTTTTCTGAGATTCCGGATGATTTAGGGGTTAGT
GCTTCTCTTATTGGTGTGTTGGGCATGATCCCGACTGCTATGTTCCGCGGATGCTGCGTTT
GCGCTTCCGTCGTTGAAGAGGAAGTTCACTACTTCCCAACTGTTGATGTTTGCCATGCTG
TTGACTGCTGCCGGTCAGATTATTCGTGTGCTGGACCTGCTTCGCTGTTGATGGTCGGT
ACTGTGTTCCGCGATGTTTGGCATCGGAGTTACCAATGTGTTGCTTCCGATTGCTGTTAGG
GAGTATTTTCCGCGTCACGTCGGTGGAATGTCGACAACCTATCTGGTGTGCTTCCAGATT
GTTCCAGGCACTTGCTCCGACGCTTGCCGTGCCGATTTCTCAGTGGGCTACACATGTGGGG
TTGACCGGTTGGAGGGTGTGCTCGCTCGGTTTCGTGGGCGCTGCTGGGGTTGGTTGCCGCGATT
TCGTGGATTCCGCTGTTGAGTTTGCAGGGTGCCAGGGTTGTTGCCGGCGCCGTCGAAGGTT
TCTCTTCTGTGTGGAAGTCTTCCGTTGGTGTGGGGCTCGGGTTGATGTTTGGGTTTACT
TCGTTTGCGACGTATATCCTCATGGGTTTTATGCCGCAGATGGTAGGTGATCCTCAGCTC
GGTGCGGTGTTGTTAGGCTGGTGGTCAATTTTGGGATTGCCGCTGAACATTCTGGGACCG
TGTTGGTGACGCGTTTCACTAAGTCTTCCGATGGTTGTTATCGCCAGTGTCTGTTT
CTCATCGGTAATGGTGGGTTTTGTTTGGCTCCGATGTTGCGCCGTGGTTGTGGGCGACG
TTGTCTGGTCTTGGTCCCTTGCGTTCCCGATGGCGTTGACGCTCATTAATATTCGTGCT
GAAACTAGTGCTGGTGTCTTCTGCGTTGAGTTCCTTCGGGCAGGGTTTGGGTTATACGATT
GCGTGTTCGGTCCCTTGTGACTGGTTTCATTGTGCGATGCGACAGGCAGCTTCCGAACA
ATCTTTGTGCTTTTTGCGGTTGCAACACTCTTCGTTATTAGAGGCGGTTACTTTGCGACA
AGGCAGGTTTACGTGAAAAGCTTTTAAATCGC

>RXN00099-downstream
TAGGATGGCGCTATGCCGCAAAG

>RXN00193
AAAGCTTTCTNCCAACGCGAAGGTTTCATCTCAGCCTTCGGTTTCACCGTCCTCGTGGTC
ATCGTCTCCGTGATCACAGTCAACATCTTCGCCTTCCTCTTGGCGTGGTTGCTGACCCGC
AAACTCCGCGGTACCAACTTTTTCCGCACAGTCTTCTTTATGCCGAACCTTATCGGCGGC
ATTGTGCTGGGTTATACCTGGCAGACCATGATCAACGCCGTGCTTTCGCACTATGCCACG
ACTATTAGCGCGGACTGGAAATTCGGCTACGCCGGCCTCATCATGCTACTTAAGTGGCAG
CTCATCGGCTACATGATGATCATTTACATCGCCGGCCTGCAAAACGTCCCACCAGAGCTC
ATTGAGGCTGCCGAACCTCGACGGCGTCAACAAGTGGGAGATGCTGCGGCACGTCACTATT
CCGATGGTCATGCCATCCATCACCATCTGCCTCTTTTTGACTTTGTGCAACTCCTTTAAG
CTCTTCGACCAGAACCTGGCGCTGACCAACGGCGCTCCTGGCGGGCAAACCTGAGATGGTG
GCGCTCAACATCATCAACACGCTGTTTAAACGTATGAATGTCGAGGGCGTGGT

>RXN00378-upstream
ACCGTGAGCCTTATACTGTGAGGACATTAAAAGTGACACCTCTTTTCTATCTTTTACAA
CCCAAGAAGGTTTATCGTGAGCACACCGGATTCTTCCTCG

>RXN00378
GTGGACAAGGCCGTAAACACTGCTATCTCTGACGCCAAAACAGCGGCGCTCAAGGCAGGT
GTTGGATTGAACCGAGCCACCGCCTCAGAAGAAGAGGAAGATTTAAGCTCAAGCATTAAG
GTTTCTTTGGCCTTTGAGCTCGAGGGGTTAAGCAATGCACCATCGTTGATGGTGGTGGAA

AAAGCCCTAGAGAAGATCCCCGGTGTATCCGCGGATCTGATTACCCCTTCACAACTGCA
 TGGATTACAGCAACTGATCGGGTACATCCCGAAACCTCATTGAGGTGTTTGAGCAGTTC
 GGCATCAAAGCACACCTTTCTAATTCATCGCTGCTGCGCAGGCATCAACAGCTCAGCGCG
 GAAGTAAATAGGGAAGCACGCCTTGATCGTTACCGCTCCCGAATGGATGCCAAGCGAATC
 TCGCCTCGTGTGCGAAGGCATAACCGACAAGAAATGGTACATGCGGTACGCGCTCGTGAA
 AGTGGTTGGATTAAACGCAGGAATCACACCACCTCGCAGCATGAAGACCCAATGTCGGGC
 GATGTGCTGTTACCGCCCCGCGCACTGATTACACCTAAGCGTTTGTGGGTGTCGTTGCCG
 TTTGCGCTCATCGTATTGGCGTTATCGTTGAATCCTTCGTGGCAGTTTGATTATTGGCAG
 TGGTTGTCCGCTGTGTTGGCTATTCTGTGGTGGTGTGGGGTGCTTGCCGTTTACCAGC
 GCTGCAGCAGGCGGTATTTCGTGAGGAATTTCCGCTCTTGATGCGACCAGCTCAATCGCT
 ATTGCTGCTGCATACGCGTGGTCTATCGCCATGCTGTTGTTTGAACCCAGGAGGTAAA
 TCCTGGCGGTCATATCCGTCCTGGTTGCTTTTGACCACGGCACGTTGACCCAAAACGAG
 ATTTATTTTGATGTGGCCTGCGGAATCACCGTGTGCTTCTTGCCGGACGGCTGCTGACA
 AGGCGTCGAAGCCAATCCAGTTTGTAGCGGAACCTGGTCGCTCCAAATCGATCCACAG
 CGCATTGTCACTGTGGTGCCTAAACACCGATTGAAGCGCGTAGTCCAGGAAGTGAACATT
 CCAGTGCAGGAAGTCCGTGTCAATGACGATGTGAAAGTTCCACCTAATACCACGATCCCT
 GTGGATGGCACTGTATCGGTGGCGGTTTCGCGGATCGCAGCTAGCATCATGCGGACAA
 GACCAGCGTGATGTAAAAGTAAATGACAAAGTTTTCGCGGCGAGCCTCAACCTCGAATCC
 GAAATCAAGGTTTCGTGTTATTTCGCACTGGTCACCGCACCCGCATCGCCGCGGTACATAGG
 TGGGTTAAAGAAGCGACGTTGAAGGAAAACCGCCACAATAGGGCAGCGATCCGTTCCGCC
 GGTAACCTTGTGCCCATCACGTTACCCCTTGCTGTGGTGGACTTCTGTCTGTGGGCACTG
 ATCTCTGGAAACATCAACGCTGCATTTACCACTACCTTGGCTGTCTTGCCTGCGTGCGTGGCT
 CCGGTGGCCTTAGCGTTGTCTGCTCCACTTGCCACGAGGAATTCATCGAAGCTGCAGCA
 CGACACGGTATTTTGGTCCGCTCTGGTGAAATTTTCCGAGTTCTCGATGATGTGGATACT
 GCCGTATTTAATCGTGTGGGCACACTAACCGATGGCGAAATGACAGTGGAAACCGTCACA
 GCAGACAAAGGCGAGGACCCAGAACTAGTGCTGCGTGTGCGCGGGGCGTTGGCCATGGAA
 TCCACACGCGGATTTCCAAAGCACTGGTGAAAGCATCCCGTGAAGCTCGTGATACCGGC
 GCCGGTGGTGAAGATGTCCACACTGGATTGAAGTAGGCAACGTGGAAATCACCGAAGCC
 GGCTCATTTCCAAGCAACCATCGAGCTGCCACTGATCAAACCATCTGGCGAAAAAATCATG
 CGCACCACAGAAGCACTCCTGTGGCGACCACGATCCATGACAGAAGTCCGTGAGCACTTA
 AGCCCCGACTAGTGGCAGCAGCAACCTCAGGTGGCGCACCAGTATCGTGCGATGGAAA
 GGCAAAGACCGCGGAGTTATCACTCTAAGTGACCACGTGAGATCAGATTCTCCGATGCG
 ATTATTGCGATTGAAGAACAAAGGCATCGAGACCATGATGCTTTACAGTGATACTTACCCG
 GTGGCAGTCGATACGCAGACAGCTTAGGCATCACCCACGCTTTGGCCGGCATCGCGCCG
 GGCAAGAAAGCCAGGTTCGTCCGTGCAGTCCACACCCGCGGATCCACTGTGCGGATGATC
 GGCGATGAATCAGTAATGGACTGTTTGAAGTGCCTGACGTGGGTGTAAGTATGATGGGCGTC
 GATCGTCCCTCAGATCTGCGTGATGATTCCGATGACCCGGCAGCTGACGTTGTGGTCATG
 CGCGAAGAGGTCATGAGCGTGCCGACGCTGTTTAAACTGGCTCGACGCTACGCCAAGTTG
 GTCAATGGCAATATTGCTCTGGCCTGGATCTATAACGGTGTGGCATGGTGCTTGCAGTG
 TCTGGCTTGCTGCATCCAATGGCTGCGACCGTGGCTATGCTGGCGTCTTCGCTGCTTATT
 GAATGGCGCTCGGGCAGGGCGCGCAAGTAC

>RXN00378-downstream
 TAACCAGCAATTCCCAAGCCCAA

>RXN00412-upstream
 CTTTGTGACGAACACCACGTGCGGTACGCTTCCCTCGGGGCGTTAAACTATTTGTCTTCCAG
 CTTTGTGCCCCGACTTTTGTACGAATCGAGGACACCGTC

>RXN00412
 GTGTCACACACCGCGTCCACACCGACGCCAGAGGAATACTCCGCGCAGCAACCCAGCACC
 CAGGGCACTCGCGTTGAGTTCCGCGGCATAACCAAAGTCTTTAGCAACAATAAATCTGCT
 AAAACCACCGCGCTTGATAATGTCACTCTCACCGTAGAACCCGGTGAGGTAATCGGCATC
 ATCGGTTACTCTGGCGCCGGCAAGTCCACTCTTGTCGCGCTCATCAATGGCCTTGACTCC
 CCCACGAGCGGTTGTTGCTGCTCAACGGCACCGACATCGTCGGAATGCCCAGTCTAAG
 CTGCGTAAACTGCGCAGTAATATCGGCATGATTTTCCAGCAGTTCAACCTGTTCCAGTCG
 CGTACTGCGGCTGGAAATGTGGAGTACCCGCTGGAAGTTGCCAAGATGGACAAGGCAGCT
 CGTAAAGCTCGCGTGCAAGAAATGCTCGAGTTGTCGCGCTGGGCGACAAAGGCAAAAAC
 TACCCCGAGCAGCTGTGCGGCGGCCAGAAGCAGCGCTCGGCATTGCCCGTGCACTGGCC
 ACCAATCCAACGCTTTTGTGTTGCGGACGAAGCCACCTCCGCTTTGGACCCAGAAACACC
 CATGAAGTTCTGGAGCTGCTGCGCAAGGTAAACCGCGAAGTGGGCATCACCATCGTTGTG

ATCACCCACGAAATGGAAGTTGTGCGTTCCATCGCAGACAAGGTTGCTGTGATGGAATCC
GGCAAAGTTGTGGAATACGGCAGCGTCTACGAGGTGTTCTCCAATCCACAAACACAGGTT
GCTCAAAAGTTTCGTGGCCACCGCGCTGCGTAACACCCAGACCAAGTGGAATCGGAAGAT
CTGCTTAGCCATGAGGGACGTCTGTTACCATTTGATCTGACTGAAACGTCCGGCTTCTTT
GCAGCAACCGCTCGTGCTGCCGAACAAGGTGCTTTTGTCAACATCGTTCACGGTGGCGTG
ACCACCTTGCAACGCCAATCATTTGGCAAAATGACTGTTGACTCACCGGCAACACCGCT
GCGATTGAAGAGTTCTATCAAACCTTGACCAAGACCACGACCATCAAGGAGATCACCCGA

>RXN00412-downstream
TGAACGAGATGATCCTCGCAGCT

>RXN00431-upstream
TGGATCGTCTCGCTTCACATTCGTCGGCCTTGGCCTTGCTCTCCTCGCGATGAAGCAA
TGGCGATTCCGCGTCAGCTACTGGGTATAAGGAGCACCAC

>RXN00431
ATGGTATCCATCGATACATACAACGCCTGCGTCGACTTCCCCATCTTCGACGCCAAATCC
CGTCCATGAAGAAAAGCCTTCTCGGCGCAGCCGGCGGAGCAATCGGGCGCAATCAAGAC
AACGTCGTAGTCGTGAAGCGCTGAAGAACGTCAACCTGCACTTGC CGGAAGGTGACCGG
GTCGGACTCGTCGGCCACAACGGCGCGGGCAAATCCACCCTCCTGCGACTCCTCTCCGGC
ATCTACGAACCCACCCGCGGAAGCGCTGACATCCGTGGACGCGTCGCCCCCGCTTTCGAC
CTCGGCGTCGGCATGGATCCAGAAATCTCCGGCTACGAAAATATCATCATCCGCGGCCCTC
TTCTCGGTCAAACCCGCAAACAGATGAAAGCCAAAATGGAAGAAATCGCCGACTTCACC
GAACTCGGCGAATACTCTCCATGCCTCTCCGAACCTACTCCACCGGCATGCGCATCCGC
CTAGCCCTCGGCGTGGTCACTCCATCGAGCCCGAAATTCTGCTTCTTGATGAAGGCATC
GGCGCCGTCGACGCCGCTTCATGGCCAAAGCCGCGACCGCCTCCAAGCCCTCGTCGAA
CGATCCGGCATCTCGTCTTCGCTCCCACTCCAACGACTTCCTCGCCAACTCTGCAAC
ACCGCACTCTGGGTGCGACACGGACAAATCCGCGAAGCGGGACTAGTTCCAGACGTGGTG
GAAGCCTACGAAGGCAAGGGCGCCGGCGACACGTCGCGAGACTCCTCACCCGCATGGAA
GAAGAAAAG

>RXN00431-downstream
TAGCTCCTGCGTTTCGGGTTTGC

>RXN00444-upstream
TACCCAATGGCATTGACCACCACCGGTGAAGACAACGAGGTAGCGAAGGCTTTCGCAGAG
TTCTTCAGCAGCGATCGTGCCAAGGAGATCCTTGCCAGCT

>RXN00444
ATGGTTTTGGCACAAACTAAAAAGGCTCGTCGAAGCGAGAATCATATCCTCCCAGGGTGG
TTGCTCATCCCAGCCACCCTGGCCATGCTGCTGATCATTGGACCTATTTTTGCTTTGCTG
TTGAGATCCCCTGGGATCGGTCTTGGGAGTTGCTTACCGCGCCGGAATCTTTAGGAACC
GCACGGTTATCTATCGGAACTGCTCTGTTTTCTACCGCGCTATGCGCAATTGTGGGTTTC
CCGCTAGCGTTGGCGCTGCATTTATATGAGCGTTTCGACCCAGGGTGACATCAGTTTTC
ACGGTGTCTGTTTATGCGCCTTTGGTGTTGTCGCCGGTGGTGTCTGGTTTGGCGCTGACT
TTTCTGTGGGGCAGGCGTGGTTTTTTAGGTTCTTGGCTTGATCAGGTTGGATTGCCGATT
GCATTTACCACCACGGCTGTGGTGTTTGCCAGGTGTTGTAGCGTTGCCATTTTTCATT
TCCACTGTGACTACTGCACTGCGTGGCATTCCAAAACAGTTTGAGGAAATCGCAGCTACT
GAAGGCGCAACCCGCTGGGAGATCATGCACAAGATGATCATTCCGCTGGCGATGCGCTGGA
ATTTTCACCGGTATGATTTTGGGATTGCCAGGGCCTTGGGCGAGTATGGTGGGACACTG
ACTTTTGCTGGAAATATTGCAGGTGTTACCCGCACCATTCGGTTGCATATTGAGCTTGGT
TTGAGTTCCAATGACATGGATAAAGCCTTGGGAGCGGTGATTATGCTTTTGGCTGTCTAT
GTCTCATCATTGGAGCCATCGGAGCGTTACGATTGTTTTCCAAGGTGAGAAAGGTT

>RXN00444-downstream
TAATTGATGTCTCGTTCCCGGA

>RXN00466-upstream
TTTAAAGCGCACTAAGAGCTCGTCAATTCTTTAAACAAGCTGAGAATGTGAATAATAG
GATAGGTTAACCTGATTGATTAGAAAACGGAGATTTGTC

>RXN00466

GTGCAATCCCCGCTGTCCAAAATCCTGCGCAGTAGCGTCGTAGGCGTTGCTGTCTAGCC
CTGTTAGCTGGGTGTTCTAACAATGCAGATGACACCGACGCTGATTCAACATCCACGGGA
AACTCCGCTTTTCTGTTCGATTGAACACGAGTTCGGAACCACCACAATCGATGATGTA
CCGAAAGAGTTGTCACCCCTTGGCGTTACCGACGCCGATATTGTCTCGCATTGGGGACC
GTCCCAGTAGGCAACACCGGATACAAATTCTTCGAAAACGGATTGGGACCGTGGACTGAT
GAGTTAGTGGAAGGCAAAGAATTAACACTGCTTGACTCTGATTCCACACCAGATCTTGAA
CAAGTAGCAGCCCTGGAGCCAGACCTGATTATTGGAGTCTCTGCGGGGTTTGACGACGTT
GTATACGAGCAACTATCTGATATCGCACCGGTGGTCGCCCGTCCAGCGGGAACAGCTGCA
TACGCAGTAGCTCGCGAGGAAGCTACCAACCTTGTTCGCCGTGCGATGGGGCAATCAGAA
AAAGGACAAGAGCTCAATGAGGAAACAGATGCTCTGATCCAAGCTGCGCGTGATGAAAT
CCTTCTTTTGACGGTAAACAGGAACCGTCATCTTGCCATACCAGGGTAAATACGGTGCC
TACCTGCCAGGCGATGCACGGGGACAATTCTCGATTCACTTGGCATTTCGCTGCCGGAA
GCAGTTCTTTTCGCGAGACACCGGCGACAGCTTCTTTGTGCGATGTCCCCGCTGAAAGCGTC
AAAGACGTAGACGGTGATGTTCTCTCGTGCTTTCCAACGACGAAAATCTGGATATCACA
GCAGAGAATCCACTGTTTGAAACACTCAACGTTGTGCAAAAAGACGCAGTAATTGTGGCA
ACAACCGAAGAACGCGGGGCGATTACCTACAACACTCAGTGCTGTCTGTTTCCTTTTGCCTTG
GAACATCTCGCACCCACGTATTGCTGAGGCTTTGAAG

>RXN00466-downstream

TAAAACTCAACTACTCGAGCACA

>RXN00523-upstream

TGGTGACTCGTCCGAGTGAAATTGCCGTGGGCATCATCATGCCGATCATTGGTGCGCCAC
TGTTTATTTGGATTATTTCGTGCTCAGAAAGTCAAAGAGCT

>RXN00523

ATGAGCCTTAGCCATCAACTCAAGCGCCAGCGCGCATCGCGCAACTCCCGCAGGTGGCTG
ATTGTTGCGGCATTGGGCGTCGTACGCTTGGTATTTTTGCTTTTTCTTTGATGTGGGGC
GAGGTGTTTTATGGCCCTGCTCAGGTGCTGAAAGTGTTGTCTGGACAGCAGGTTCCTGGC
GCGAGTTATCCGTTGGCGTGTTGCGTTTGGCGCGCGCGGTGATGGGTTTGAAGTGGGGT
TTGGCGTTTGGCGCGCGCGGTGATTTTTTCAGACGGTGTTGCGTAATCAGTTGGCGTCG
CCGGATATTATCGGCATTTCTTCTGGCGCGTCGGCGCGGGCGTAATTTGCATTGTGTTT
TTCGGGATGTGCGAGTCTGCAAGTGTGCGCGATTTCTTTGTGTGCGTCTTGGCTGTGGCG
TTGTTGATTTATCTGGTGGCGTATCGCGGTGGTTTTTCGGCCACGCGTCTGATTCTTACC
GGCATTGGTATTGCTGCGATGCTGAATTCATTAGTGTGCTATTGCTGTCCAAGGCTGAT
TCTTGGGATCTGCCGACCGCGACGCGTGGCTTACCGGCTCGCTCAATGGTGCGACGTGG
GATCGTGCGATGCCGCTGATTGTCAACACTGTGGTACTCATTCCGCTGCTGGTGGCTAAT
GCGCGCAATGTGGATCTTATGCGTTTGGGCAATGATTCCGCGGTGGGTTTGGGCGTTGCT
ACTAATCGCACGCGCGTCATTGCGATTATTGCCGCTGTTGCGCTCATCGCCGTTGCTACC
GCTGCATGCGGCCCCGATCGCATTCGTGGCGTTTGTGTCTGGCCCCATTGCCGCGCGCATT
TTAGGCTCCGGCGGATCGCTCATCATCCCTCCGCACTCATCGGCGGGTTGATCGTGCTC
ATCGCCGACCTAATTGGCCAATACTTCTCGGCACCGCTACCCCGTCCGAGTTGTCACC
GGCGCATTCGGCGCCCCATTCTTATCTATTTACTCATTCGTTCCAACCGCGCGGGAGTA
ACCTG

>RXN00523-downstream

TGACCACCAACCATCAACTATCC

>RXN00525-upstream

CCATCGTGTTTATTACTCACAACCCTGAGCTTGCTGATGAATCTGATCGGGTGGTCACCA
TGGTTGACGGGCGCATCATTGGGTCTGAGGTGAAACACTC

>RXN00525

ATGAGCCTTGAGAATCAATTCTTTTGGCGCTCACCAGCCTGAGAAGCAACAAGATGCGT
GCATTGTTGACGCTGTTAGGAGTCATCATTGGTATCGCATCAGTCATCGGAATTTTGACC
ATTGGTAAAGCCCTGCAGGATCAAACCTTTGAATAGTTTGGAAAGCTTGGGCGCGAATGAT
CTGTGCGGCGAGGTGGAGGAACGCCCCGACGAAGATTCCTCCGAACCCGATATGTTCCGT
TTTTCTGGGGCTGCAAACCTCTAGTGGCAATCTGATTCCGGAAGAAACAGTTGATACGCTG
CGCGATCGTTTCGCGAGGAGCATCACGGGAATCAGCGTTGGCGGAATGGGTACGCAAGGC
ACTCTCATCGGCGACACCGCAGATCTTAAATCCGATCTCCTCGGCGTCAACGAGGATTAT

ATGTGGATGAATGGCGTCGAAATGAACTACGGCCGCGCCATCACGCAAGACGATGTTGCC
 GCTCAGCGCCCCGTTGCGGTTCATCGCCCCAGACACCTTTAATACGCTTTTCGACGCAAAC
 CCCAACCTCGCTCTGGGGTCCGAAGTAGCTTTTGAAGTCAACGGTCAAGAGACATTTTTCG
 CGGGTTATCGGTGTGTATAAAGAAGCCGCGAGAGGTGGACTTGTGGGAAGCAATCCAACC
 GTCCACACCTACACCCCATATACGGTGGCCAATGACATCACCCACACGGAAGATGGATTG
 AACACGTTAAGTATCCGTGCAGCTCAGGGCGTAGACCAGGATTCACTTAAGGGTTCACTG
 CAAACCTACTTCGACGCGCTGTACGCCAACAATGACTCGCACCACGTGGCCATGTTGGAC
 TTCCGTAAACAGATCGAAGAGTTCAACACCATTCTCGGCGCAATGAGTTTGGGTATCTCA
 GCCATCGGCGGAATTTCTTGCTTGTGCGGTGGCATCGGAGTGATGAACATTATGTTGGTG
 TCTGTACCCGAGCGAAGCCGCGAAATCGGTGTCCGAAAAGCCCTCGGCGCTCGTCGACGT
 GACATTGCGCTGCAATTGCTGCTGAAGCCATGATCATTTGTTTCATCGGTGGCATCCTC
 GGGCTGCTTTTGGGCGGCATTTTGGGATTGATCATGTCCAGCGCTATTGGCTACATTTCC
 TTGCCACCACTGAGTGGAATCGTGATCGCCTTGGTATTTTCCATGGCTATCGGCCTGTTT
 TTCGGCTACTACCCCGCCAACAAGGCAGCAAAGCTCGATCCAATTGACGCCTTGCGTTAT
 GAG

>RXN00525-downstream
 TAAAAGCCTCGTTTTTAAGGTAG

>RXN00702-upstream
 TGGCGACGATGCCAGGATTCTTGACGCCCCGCTTGCCGAAGAACAAGTGAGGGTCAAGC
 GTCGAAAAGCAATAAATAGCCCAGAAAGGGCCGAAGTTTA

>RXN00702
 ATGAGTGCTCCTTTTAGCGCGCGCACTGCGTGGTTCGACGGACCCCGTGCTGGAAGTGGAA
 AGCGTCGCTGCCTCGTATTATGACGATGAGCGCACGCTGGCGGGCGCCGAGATCAGCGAC
 GTGAATCTGACGCTTTTGAAGGCGAAATCCTGCTGTTGTGGGGCGCACCGGCTCCGGC
 AAATCGACGCTGCTGAACGCGATGTCCGGCGCGATGCCGATGCGACCGGCGGGCCGACTT
 GATGGGCGCGTGCGCGTGGTTCGGCCGGGATACGCGTGATTTCCACCACGCATGCTTTCC
 GACGTGGTTCGGCTCGTTGGGCAAGATCCGGCGGCAAGTTTTATCACCAACACGGTTGAA
 GAAGAACTTGCCTACAGCATGGAGCAATTAGGGCTCCACCTGCGGTTCATGCGCAAGCGC
 GTAGAGGAAACCCCTTGATCTTTTAGGCATCGCGGAGCTGCGATACGTGCCATTGGCGGAA
 CTATCTGGTGGTGAGCAGCAGCGGTGGCGATTGGCGCGGTGCTGACCACTCGCCCCGCG
 CTGATTATCTTGGATGAACCAACCAGCGCTTTGGACCCTAATGGTGCCGAGGATGTGCTG
 GCAACCGTAACCAAGCTGGCTCATGACTTGGCGATGACCGTAGTGCTTGCTGAACACCGC
 ATCGAGCGCGTACTGCAGTACGTGGACCGCGTGGCGCATGTGGGCGCTGATGGGCACGTC
 ACTGTTGGGACGCCGGAAGAAATCATGGCTGATTCTGATGTGGCACCACCCATTGTGGAA
 TTAGGACGCTGGGCTGGCTGGGCTCCCCCTACCGCTATCGATCCGCGATGCACGCGCACAC
 TCCGCTGACATGCGCAAACGCGTGTATCAGCGTGGTTTTAGTGGTGAACAAATTACACAAC
 CACGCTGTCCAGCCACTTTTGATCGCCGAAGATATCATGGTTGATTTCCCCGAAATCCGT
 GCCGTTGACGGCGTGAACCTGAATCTCAACTCCGGTGAAATTACCGTGCTCATGGGCCGA
 AACGGCTGCGGAAAATCATCCCTGCTGTGGGCTTTACAAGGTTGAGGGACTAGAAATCAG
 GGCTCGGTGACAGGTGCTTGATGAGGCCGCGGGATTTTCGTGGACAGACCCCAAACTTTA
 AAGCCCGCCAAGCGGCGCAATCTTGTGTCCATGGTTCCGCAAACACCGACCGATATTTTG
 TATGAATCAACCGTGCATGCAGAGCTCGCACGCTCTGATAAAGATGCCGAGCACCAGCC
 GGCACACGCGGGAAATCCTGGATTCACTGGTCCCGAATATCCCGGACCATCTCCACCCA
 CGTGATCTATCAGAAGGCCAAAAGCTCTCCCTCGCGCTGTCCATCCAACCTCGCCGCAAAA
 CCCCAGCTGGTATTTTTCGACGAACCCACCGCGGCCTAGACTACGACGGCAAGAAATCC
 CTCGCCCCGCTCCTTCCAACAACCTCGCAGACGACGGCCACGCCATTTTGGTGGTCACCCAC
 GACGTGGAATTCTCTGCACTGTGCGCCGACCGAGTGTTGTTTATGGCCTCTGGAAAGATC
 ATCTCCGATGGCACAGCCGTAGAAATCCTCCCGCATCACCGGCTTACGCCCCACAAGTC
 GCAAAAATCACCGCCGGCATCCAAGAGGAATCACACTGGCTCACAGTCTCGGCCGTGAAA
 GCTGCGCTAGGGCATGGTGAAATCTCA

>RXN00702-downstream
 TGATCAACGCCATCACACTCAAG

>RXN00726
 AACGCGGGTCGCTTGTATGTGATGGCGATCTCATTGGCTACCGAGAGCGCGATGGCGTG
 CTGTACGAAATCTCTGAGAAGGACGCCGCCAAGCAGCGCTCCGATATCGGCATGGTGTTC
 CAGAACTTCAACCTCTTCCCCACCGCACGGTGATCGAGAACATCATCGAAGCTCCCATC

CACGTGAAGAAGCAGCCCGAAAGCAAGGCCCGCGCACGTGCCATGGAGCTGCTTGAGCAG
 GTCGGCCTCGCCACAAAGCGGACGCGCTACCCCGTCCAACGTGTCGGGTGGTCAGCAGCAG
 CGCGTTGCAATTGCCCCGCGCCGTGCGCATGGAGCCAAAGCTCATGCTTTTCGACGAACCC
 ACCAGCGCTTTGGACCTGAACCTCGTCGGTGAAGTCCTGCGAGTGATGAAACAGCTCGCC
 GACGACGGCATGACCATGCTTGTTGTACCCACGAAATGGGCTTCGCCACGAAGTCGCC
 GACCAGGTCGTGTTTCATGGCCGATGGAGTTGTGCTTGAAGCCGGAACCCCCGAACAAGTT
 CTGGACAATCCAAAGGAACAGCGCACCAAGACTTCCTGTCTTCTCTGCTC

>RXN00726-downstream
 TAACCTTTTCGGGTCTTAAAAA

>RXN00732
 AATCACCTCCTCTACTCCCCACGGTAAAGGCAGACATCATTGACAATGGTGTGGTCACA
 GGTGACATCGGCTATATTTGGCAGACCGGTGGAATCATGCTGGCCCTGACATTAGTCCAG
 GTTGCCCTGCGCTATCGCCGGTGTATTTTCGGTTCCAAACTATCCATGAGAGTGGGCCGC
 GATCTGCGTTCGGCGATCTTTGGCAAGGTAGTGAACCTCTCTGAGCGTGAGATGGGTGAG
 TTTGGCGCACCGTCGCTGATCACCAGAAACACCAACGATGTGCAGCAGGTTTCAGATGCTG
 GTGCAGATGACCTCCACTTTGATGATTTCCGCCCCGATGCTGGCCATTGGTGGCATCATC
 ATGGCGGTGCGTCAGGATCTTGGTTTGTCTTGGCTGATGGTGGTCAGTATTCGGGTGCTC
 ATCATCGTGGTGGCGCTGATCATTGTGCGCATGGTTCCGTTGTTCCAAACCATGCAAAAG
 CGCATTGACCGCATCAATCAGATTATACGCGAGCAGCTCACCAGGTATCCGCGTGATCCGC
 GCGTTTCGTGCGTGAAGATGTGGAACGCGAACGATTACCACTGCTAGTAAAGATGTCGCT
 GATATCGGCGTGCGCACCGGTAACCTGATGGCGTTGATGTTCCCTGCCGTGATGCTGATC
 ATGAACCTTTCTGCCGTTGCTGTGATTTGGTTTGGTGTCTTCCAGGTGGAATCCGGCGAG
 ACGCAGATCGGTACGCTCTTTGCATTCTTGCAGTACATCATGCAGATCCTCATGGGCGTC
 ATGATGGCAGCGTTTCATGTTTGTCTGATGGTTCCGCGCGCTGCCGTTTCCGCTGATCGCATC
 GGTGAGGTTCTGGAACACACCGCTCTGTGCAGGCGCCAGAAACACCGGCGCAGCCGTGCG
 ACAAGCGCTGGCGAAATCGTGTTCAACAACGCGACTTTTGCCTACCCCGGCGCGGATGAC
 CCCGTGTTAAATAATGTGAGCTTCCGCGTTGCGCCTGGTAGCACGACGGCGATCATCGGC
 TCGACGGGTTCCGGTAAGACGACGTTGATCGGGCTGGTTCCCTAGGCTTTTCGACGTCACC
 GAAGGCGACGTTACCGTCGATGGCACCGATGTTTCGTGAATTTGAGCCGCTGAAGCTGTGG
 GATCGGATCGGTCTTGTTCGCGAGAAGTCGTTCCCTGTTTCTGGAACGATCGCCAGCAAC
 CTGCGTTATGGCAATGAAGATGCCACGGAACGCGAGCTGTGGCAGGCGCTTGCAATTGCT
 CAGGCGGCGGACTTTGTGCGTGAGATGCCAGAGGGTCTTGATTCTGAGATTGCTCAGGGT
 GGAACCAATGTTTCTGGTGGTCAGCGCCAGCGACTAGCCATTGCCAGGGCGTTGTTGAAG
 CAACCTGAGATCTATATTTTCGACGATTCTTTCTCCGCCCTCGATGTGAGCACAGACGCC
 GCTCTTCGCCGAGCGCTGAGCACCAACCTGCCGGATGCAACCAAGTTGATTGTGCGCCAG
 CGTGTCAGCACGATTTCGAGATGCCGATCAGATTGTGGTGTCTGATAACGGCGAGGTTGTC
 GGTATTGGAACGCACACGAATTTGCTGAACACGTGCGGTACCTACCGTGAAATTGTTGAA
 TCCCAAGAGACTGCGCAGGCGCAATCA

>RXN00732-downstream
 TGAGTAATACTGCAGGCCCGCGC

>RXN00759-upstream
 TCACCTTGAACACTTAAACATAACTTCATCCGGCGCTTTATTAGCTTGAAGCGCCCCGC
 ACCATAATCCATTCCCCAGCAAGCAAGGACACCCACGCTC

>RXN00759
 ATGCTTCGTTACGTGCGGCGACGTTTGCTCCAAATGATTCCGGTCTTTTTTCGGAGCGACC
 TTAATGATTTACGCCCTCGTGTTCTCATGCCTGGTGACCCAGTCCAGGCATTGGGAGGT
 GACCGCGGCCTAACCGAGGCTGCGGCCGAGAAAATCCGTCAAGAATACAATCTTGATAAA
 CCCTTCATCGTTCAATACCTCCTGTACATCAAGGGCATCTTCGTCTTAGATTTTGAACA
 ACCTTCTCTGGTCAGCCAGTTATTGATGTGATGGCCAGGGCCTTCCCCGTACCATCAAA
 CTCGCCATCATGGCCCTGCTGTTTGAATCAATCCTCGGCATTATCTTTGGTGTATCGCA
 GGTATTCCCGCGGAGGAATCTTCGACTCCACCGTGCTGGTCCTTTCTCTGATAGTCATC
 GCAGTCCCCACCTTCGTCAATTGGTTTTCGTGCTGCAGTTCTTAGTCGGCGTGAAATGGGGC
 TTAATGCCCCGTACCGTAGGTTCCAACACATCAATAACGGCGCTGATCATGCCGGCTGTC
 GTACTGGGTGCAGTATCGTTTCGCTTACGTTCTTCGCTCACCAGACAATCCGTGAGCGAA
 AACCTCCGCGCTGATTACGTTTCGAACCGCTCGAGCAAAAGGCATGTCCGGATTCAACGTG
 ATGAACCGCCATGTGCTTCGAAACTCACTGATTCCCGTTGCCACCTTCTGGGCGCCGAT

CTCGGTGCACTGATGGGTGGAGCGATTGTACCCGAAGGTATCTTCGGCATCAACGGTGTG
GGTGGAACGCTCTACCAGGCCATTTTGAAAGGTGAACCCACCACGGTTGTCTCCATTGTG
ACTGTGCTGGTCATCGTCTACATCATCGCCAACCTTCTCGTGGACTTGATCTACGCCGTT
CTCGATCCGAGGATCCGCTATGCC

>RXN00759-downstream
TAATAATGAATTCCACACAAACC

>RXN00808-upstream
CGCGATGTCGCACCGGCACGTTAGAGTATTGAGCATGAGTCGATTGCTTAGAGCATTGAA
ATGGCTGTGGGGCACATCGTGGCCGCTGTATGCTGCGACG

>RXN00808
GTGCTCGGCACGAATGTGTTTGGTGCGCTCGCAGTAATGCTGTTTGTGCGCTTCTCAT
CCGCAGCCAGATGCTTCAAATTTCAACGCTGAGATCTCGTATCTGCCAGCTGTTGGTTTC
GCATACCTGGCGTTTCGCCATTTGTCGCGGGCATGCTGGTGACATTTTGTATGTTCCGCCCCG
GTGCTTGATTGGCAGCGAAGCCCTGAAGATCATGACCGAAATATGGTGCGCAACTTGGTT
ATGCGCATCCCCATCTACCAGGCAATTCTGTGCGCAGTGGTGTGGTTAATCGGCATTGCA
ATTGCAACGTTGATTTTCGGCCAGTGTGTCTACCAGTTTGGCGCTGGTTCGTGGCGTTTCC
ACGTTGATGGCTGCCGCAATCGTCTGTGCTGCTCACCTACCTTGAGGCTGAGCGTTTGGTG
CGTCCGGTTGCTGCGTCTGCCCTGGCGCGTTCGATTTGAGGATTCCACGCTGGAACCACT
GTGAGCCAGCGCTTGGCTATGACGTGGTTGCTGACGTTGGGCATTCCAGTGATGGGAATT
CTGCTGCTTATTTGGGGCTACTCGCAGGGCATTTCGGCTCTGATGCCTCCGGAATTATG
CCTGCCATCGCAGCGCTCGCGTTTGCATCGTTGGTCACGGGTTACCTGGGCAACCGGCTT
GTGGTGCTCTGTGGTGGATCCGATTTCGGGAACCTTCAGGAGGCCATCAACAGGGTTCGT
CGTGGTGAAAACGATGTGCAGGTTGATATTTATGATGGCTCTGAGATCGGTGTGCTTCAG
GCTGGCTTCAATGAGATGATGCGTGGCCTGCGTGAACGTGACGCGCTCCGTGACCTTTTC
GGTCGCTACGTGGGCGCTGAAGTGGCCAAGCGTGCGCTGGAGGAACGCCCCACTCTGGGT
GGCGAGGACCGTAAGGTTGCCGTGTTGTTTGTGCGATGTCATCGGCTCCACTACCTTTGCC
GTCAACCACACTCCTGAAGAGGTTGTGGAGGCGCTCAATGAGTTCTTCGAGCACGTTCGT
GAGGTTGTGCACCGCAACAAGGGTGTTATCAACAAGTTCCAGGGTGACGCGCGCTTGGCG
ATTTTCGGCGCTCCCCCTGCCCTGTCTGATGCCACCGGTCATGCGCTTGGCGCTGCCCGT
GAGCTCCGCGCAGAGCTGAAAGATCTCCAGCTCAAGGCCGGAATTGGTGTGGCTGCTGGC
CATGTGCTTGTGTCATATCGGCGGTCACGCGAGGTTTGAAGTACTGTGATCGGCGAC
GCGGTGAACCAGGCTGCGCGCCTGACGGAGATCGCGAAAACGACCCAGGCCGACCGTC
ACCAACGCTTCCACGCTGCGTGAGGCCAACGAGGCGGAGCAGGCTCGCTGGACGCTCATG
AAGTCCGTGGAGCTGCGCGGACGTAGCCAGATGACGCAGATTGCGCGGCCTATTTCGGCCG
ACGTTGGCGGATAGGTCC

>RXN00808-downstream
TAATACGCTTTTCGACGCAAAAA

>RXN00828-upstream
CGGTGATCACCGGGCCGAATGGCGCTGGAAAATCCACACTTGCGCTGACCATGGGTGGAT
TGCTTCCGCGAAAAGTGGGCAGCTGGAACCTCTCTGACACG

>RXN00828
GTGCGCGGCGGCCTTAACACGCCCCCGCACAAAGTGGCGTTTCAGCTGATCTAGCTGCACGT
ATTGGCACTGTCTTTTCAGGATCCAGAGCACCATTGTTGGCGCGCACTGTGCGTGATGAG
CTAGAAATTGGGCCGAAAATCATGAAAGTCGATGCAAGCGAGCGCATCGAGGAGCTGCTT
GATCGTTTGCCTCCGCCACTTGGAACGCAATCCGTTTACCTTGAGTGGTGGAGAA
AAGCGCCGCTATCTGTGGCGACAGCCTTGGTGGCAGCACCGAACTTCTCATTTTGGAT
GAGCCTACGTTTGGCCAAGATCCCGAGACCTTCACAGAGCTGGTGACGATGTTGCGTGAA
TTAACAGACAACGGAATCAGCATTGTGTGCGTAACCCATGATCCTGATTTTCATCGCAGCG
CTGGGCGATCACCATTTGAGGTGAGCGCGAAG

>RXN00828-downstream
TGAACCTGCTGATCAAAAATTAAT

>RXN00832-upstream
GAGATTGTGCTAGGTTCTGATGAGGCTTCGGGACGACCCGAAGAAATCTATGACAGCCTG

GGAACGGCCCAGAGTTCTTAAGAAAGTTTGA CTAGAGAAC

>RXN00832

ATGCCGTTTTCTTGGCTAAAACCAATTGATTATGCCCGCATCTTTGTCGGCTGGGCATCG
ATTTTTATCATCCCCCTCATCACACTGCCATCAATTATTGAGTTGGCGCTGATCGTGGCA
GTCATCCTATTCTGCGCATTTGGCGTGGTGAAGATGGCGGAGCGTTTGGCTCATATTTTG
GGTGATCCTTTTGGATCGTTGATCCTTACCTTGTGATCGTGATCATTGAAGTGATTTTG
ATCTGTGCGGTGATGCTGGGGCTGCTGATTCAACCACTGCTGGTGGGATTCCGTGATG
GCAGTGTCCATGATCATCATGGGTTTGGTCGTGGGATTGTGCCTACTCATTGGTGGTTTA
AGGCATGGAAGCATGCCACACAATGGGGTGGGAACCTCCGACCTACTTGGTGCTGATCGCA
ACTTTTTCCGTAATCGCCTTTGCGGTTCCAGCTTTTCAGGGGAGAATACTCCACTGGGCAG
GCACTTGTTATTTCAACACTGACAGCAGTGGTGTACGGGTTCTTCCTGTTTCGCCAAATG
GGTGCCCAAGCTGGTGAATTTCAAGAGGTCGAGGTCGCAGAAAAGGCAGACGACGCAGCA
AAATGGGAGGTCCCATTAGAGGCTTAATCTTGATTATCACTGTGCTCCCCATCGTGTTG
CTGTCCCATGACATGGCCACGGTGATGGATGAAGTCCTGGCAAGCCTTGGTGACCCCGTA
GCAATGGCTGGATTAATTATTGCCACCATTGTCTTCTTGCCAGAGACCATCACCTCCTTG
AAAGCTGCGTGGACAGGAGAGATTACGCGAGTAAGCAACCTCGCGCATGGAGCCCCAAGTA
TCAACGGTGGGGCTGACAATCCCAGCTGTTCTAGTGATCGGCGTGATCACAGGTCAAGAT
GTAGTTTTGGGGGAGACCCCGATCAACTTGTTGCTGCTGGGAACCAACCATTCGCGTGACA
GCCATTGCGTTTAGCTCCAAGAAAGTCAGTGCTGTGCATGGCTCGGTGCTGCTCATGCTT
TTCGGTGTTTACATGATGAGCATGTTTCGCC

>RXN00832-downstream

TGATTTAGGTAGCCTGGTGGGAA

>RXN00934-upstream

CCAACCCCTGTGGTTTGGTGATTTGGATCCGGAGCGTCTCAAGCGCTCTAGGGAGCAGAC
AAATGTTTCAAAACCGGTGGCATTACAGGAGGACAATTAG

>RXN00934

GTGCGAATTGGAATGGTCTGCCCGTACTCCTTCGATGAGCCGGGCGGTGTTCAAGCGCAT
ATCCTTGACTTAGCGCGAACCTTCATTGCCCAAGGCCATGAGGTTTCAGGTGCTTGGTCCG
TG TAGTGCGGATACGCAGGTGCCCGATTTCTGTGGTGC GCGGTGGTGGCAGCATCCCGATT
CCGTACAATGGCTCGGTTGCCCGCTTGAGCTTTGGGCCGAAAATGTTCAAGGCCGTGCGC
ACGTTCCCTCCGCGAAGGCAACTTCGATGTGCTGCATATCCATGAACCGAATTCACCAAGT
TTTTCCATGGCGGCGCTACGCTTTGCGGAAGGCCCATCGTTGCTACTTACCACGCCTCC
AGTAGCGGATCGAAGCTGCTCAAGGCTTTCTTACCAGTGCTTTTCGCCCATGCTGGAGAAA
GTGCGCGCAGGCATCGCCGTGTCTGAAATGGCTCGGCGCTGGCAGGTGGAGCAAGTCGGC
GGCGATCCCGTGCTGATCCCCAACGGGGTAGAGACCTCCATGTTCAAAGCCGCGCGCCAA
ATCGAACCGAATGATCCTGTAGAGATCGTCTTTTTGGGTGCGCTCGATGAGTCCCGCAAA
GGCCTCGACATCCTCCTGCGCGCTCTGACCAGGCTGGATCGCCCGTTTACCTGCACCGTC
ATTGGCGGCGGCACCCCGCGAGAAGTCGCCGGCATCAACTTTGTGGGCCGCGTCAGCGAT
GAGGAAAAGGCAGCAATCTTAGGTGCGCGAGACATCTATGTGCGACCCAACACCGGCGGC
GAAAGCTTCGGCATCGTGCTAGTTGAAGCGATGGCCGCGGGATGCGCTGTGCTCGCCAGC
GACCTAGAAGCGTTCTCCCTGGTCACCGATTCTGAAGCCGCACAGCCAGCGGGCGTGCTA
TTTAAACCGGCTCAGACGCCGACCTAGCCAAAAAATTCAAGCGCTTATCGACGACCCC
TCCTCCCGTTCCACGCTTATCGCCGCGGGGCTAAAGCGCGCAAACGCCTACGACTGGTGC
ACAGTATCCACCCAGGTGATGGCAGTCTATGAAACCATTCGATCGACAAAGTGAGGCTT
GGA

>RXN00934-downstream

TGACCCTTGTTTACCTCCTCATC

>RXN00939-upstream

GAATTCACCCCTGGACAAAGATCATCCACCGTGTCGAAGACGCCCAGG

>RXN00939

ATGACAAGGCAAAAAACCAGCCGTTCCCTGGAGAAATTCTCGAAGTACTACACCCCGGGC
GTCATGATCGCCGCCCTGGCCGTGCGCCTGATCACCTGAACGTTGAACTGGCCCTGACC
CTGCTGGTCATCGCCTGCCCGGTGCCCTGGTCATCTCGATCCCGGTCTCGATCGTCCGC

GGTATCGGCCGCTCCGCCAAGGACGGCGTCTGATCAAGGGCGGGGAATACCTGGAGACC
 TCCGCGAAGGTTCGACACCGTAGTCGTCGACAAGACCGGCACCCTGACCAACGGCCGCCCC
 GAGCTGACCAACGTTCGACGTCTTGGACCCCGCTACTCGGACGATGAGGTGCTCACCCTG
 GCCGCCCGCGCGGAAACCGCTCCGAGCACCCCTGGCCGAGGCCATCATCCGCGGCGCG
 GAGAACAGGGGCTTGACCGTGGCGATGGTAGAAAAGGCCGAACCGGTTCGCCGGCGCGGC
 ATCCGCGCTGACGTGGACGGTGCCACCGTGGCCGTGGGCTCAGCCGACCTGCTCGATCAC
 ACCCGGATAACACCGCATTCCTCGAGCTCAACGAACAGGGCAGGACCGCCATGTACGTC
 GGCATCAACGGCAAGGCCGTGGGCATCGTCGCTGTGGCCGACACCATCCGAGATGATGCC
 CCGGCCGCGATCAGGTCCCTGCACAATAAGGGAATCCGCGTGGTCATGGCCACCGGTGAT
 GCCGAACGCGTTCGCCCGCAACGTTCGCCCGGAGCTCGGTGTTCGATGAGGTGAGGGCAGAA
 CTGATGCCTGAGGACAAGCTCGAGATCGTCAAGGAGCTGCAGGCGCAGGGCCGGGTCTGTG
 GCCATGGTTGGCGACGGTGTCAATGACACCCCGGCACTGGCCACCGCGGACATCGGTGTG
 GCGATGGGTGCGGCCGGTTTCGCTGCCGCCATCGAGACCGCCGATATCGCCCTGATGGCC
 GACAAGCTGCCGCGGCTGCCCTACGCCCTGGGTCTGGCCCAGCGCACGGTGCGCACCATC
 CGGGTCAACATCGGCATCGCCCTGCTCACTGTACGATCCTGCTGGCCGGTGTCTGCTC
 GGTGGAGTGACCATGTTCGATTGGCATGCTCGTCCACGAGGCCTCCGTCCTGCTGGTCATC
 GCGATTGCGATGCTCCTGCTGCGCCCCACCCTGAAGGAAGACAAGGACAAGGCAGACGTC
 AGTACTGCTGACGCCGCGAAGGAGACGCTGAGCGCC

>RXN00939-downstream
 TAACGACACAATCGCCACAGCCA

>RXN00960
 ATGGCTCGGCATTGTTGCAGCAATCGCTACGCGTCCACCGTCTTCTCCGGTCTGATCGCC
 TACGGAGCATCCCAAGCGCTCTACCCATGGCTGCTGAAAGACCACCAAAGCGTCACCGAA
 ATCGACCTTGATGCAGGTGCCCTCCAGCCCTACTTCAACATCGAGATGCCACCACCATTT
 GAAGTGATGACCGCACTGCTGCTGGCATTCTGCCTCGGCCTGGGCATGGCTGTAATTAAA
 TCAGACACCCTGTTCAAGGTAACCCGCGAACTCGAGCGCGTAGTCATGAAGACCATCACC
 GCCTTTGTATCCCACTGCTGCCACTCTTCATCTTCGGCATCTTCTCGGCATGGGCATG
 AACGGTGGCCTCCTGGAGATCATGTCCGCCTTTGGCAAGGTACTGATTCTCGCCGTCTGTG
 GGAACCCCTGCTCTTCTAGCCATCCAGTTCATTATCGCTGGTGCAGTATCCAAGAAGAAC
 CCATGGAACTGTTCAAAAACATGCTCCCTGCATACTTCACTGCACTGGGCACTTCTCT
 TCAGCGGCAACCATCCCAGTGACCTACCAGCAGACCCTGAAAAACGATGTTGATGTCAAC
 GTCGCAGGCTTTGTTGTCCCACTGTGCGCCACCATCCACCTAGCTGGATCGATGATGAAG
 ATCGGCCTCTTACCTTCGCTGTTGTCTTCATGTACGACATGGAAGTAGGCGTCGGCCTC
 TCCATCGGATTCCTCCTCATGCTGGGCATCACCATGATCGCCGCACCAGGCGTTCCCGGC
 GGAGCCATCATGGCAGCAACCGGCATGCTGGCCTCCATGCTCGGATTC AACACCGAACA
 GTGCCCTCATGATCGCCGCTTACATCGCGATTGACTCCTTCGGCACCGCAGCAACGTC
 ACCGGCGACGGCGCAATCGCAGTCATCGTGAACAATTTCGCCAAGGGCCAGCTGCACACC
 ACTTCCCCAGATGAAATCGAAGAAGACGACCGCGTTGCCTTCGACATCACTCCATCGGAT
 GTGGAACATCACAAG

>RXN00960-downstream
 TAGAAACCCGCATTTTCTGTAGT

>RXN00980-upstream
 AGAGAGAAAGGGAGAAATCATGAAAACGTGGAAGACCTGGGGGGTTCGTCGGAGCTTCAGG
 CCTCTTGATTATTTTGTCTGGTTGAGTTCATCGAGCCCG

>RXN00980
 ATGCTGGCAGATGCATTTCATGATCGCGGCTGCAATTGTTGCAGGTTGGCCGATCGCGCAG
 TCTGCATATCAAGCACTTCGCATTGCAATGGTGTGATTGACTTACTGGTTCGTTGTGGCT
 GCCGTTGGTGCCATGTTTCATCAACAACTATTGGGAGTCTGCGGCGGTGACGTTCTCTTT
 GCCCTTGGCAAGGCACCTGGAACGCGCGACAATGAACCGCACACGAAAAGCACTATCGGAT
 CTGGTGGATGCAGTCCAGAAACTGCAACAAGGCTCAACGCGGATGACTCAACAGAGGTA
 GTTGAGCTGTGGGAGCTTGAGCCCGGTGACATCGTCTTGGTACGCAATGGCGAACAAATT
 CCCGTCGATGGAACCGTGATTGCGGGTGTGCGTGGAAATTGATGAATCCAACATCACGGGT
 GAATCAATGCCGGCTGAAAAGGGTCAAGGCTCTGATGTGTATGCAGGAACCTGGCTGCGA
 TCTGGTGTTTTGTAGAGTCGAGGCAACAGGAATTGGTTTCAGACTCAACTTTGGCAAAAATC
 ATTACCGCGTTGAAGACGCCCAGGATGACAAAGCCCGCACACAAACATTTCTTAGAGAAA
 TTCTCTAAGTGGTACACCCCGGCGTCATGATCGCCCGCGCAGTGGTGGGACTTATCACC

TGGGACGTAGAACTAGCACTGACGCTCTTAGTGATCGGCTGCCCCGGCGCGTTGGTTATC
 TCCATCCCCGGTGTCCATCGTCGCAGGCATCGGCCGTGCTGCACGCGATGGCGTGCTGATC
 AAGGGTGGAGAATACCTAGAAACCGCCGCGAAAGTCGACGTCGTTGTCGTGGACAAAAC
 GGAACGCTGACCACCGGCCGCCAGAACTCACAGACGTAGAAGTCATCGAGCCCGCCTAC
 AGCCAGGGCGAGGTGCTGGAGCTCGCCGCGCGCGCCGAGACGGCTTCAGAACATCCGCTT
 GCCGACGCCATCATCCGTGGTGGCCAGGATCGGGGGCTGTCCACAACATTGGTGGAAAGCA
 GCTGAAAACATCACCGGCCGAGGCATTATCGCAAATGTTGATGGACAGGCAGTTGCTGTT
 GGATCTGCTGAGTTACTTGATCATGAACCAGACTCGACCAGGATCCTGGAGCTAAATGCC
 GAAGGAAAGACCGCGATGTTTGTGCGAGTGAACGGACACGCCATTGGAATCGTGCCGTC
 GCCGACGCCGTTTCGTTTCAATTCTGCCTCAGCAATCGAATCGCTGCATAAGGCGGGCATT
 CAAGTTGTCATGGCGACTGGCGACGCTCACCGCGTTGCACAAAACGTGGCCTCCAAGCTG
 GGAGTGGATGAAGTCTACTCAGAGCTACTCCCTGAACAGAAATTAGAAGTGGTGGCTGAT
 CTGCAAGCTGCCGGCAAAACGGTCGCGATGGTGGGTGACGGAGTCAACGACACCCAGCA
 TTGGCAGCTGCTGATATCGGAGTAGCGATGGGCGTGGCAGGTTCCCTGCAGCCATTGAA
 ACCGCTGATATCGCACTCATGGCGGATCGTCTCCACGGCTGGCACATGCAGTGACCTTG
 GCAAAACGCACCGTAAGAACCATGCGCATCAATATTCTGATTGCGTTGGCTACCGTGATG
 GTGTTACTAGCTGGCGTCCATTGTCGGAGTTACCATGTGCGTTGGCATGCTCGTTTAC
 GAAGCAAGCGTGCTGCTTGTATCAGCATCGCCATGCTGTTGCTGCGTCCAACACTTAAA
 GAAGATGCTGCGCAAGCAAGTGATATTAAACGCTCGGAAATACAACAGATCGCA

>RXN00980-downstream
 TAACCAATGGCTGGGTACTGATG

>RXN01000-upstream
 CTTTCTATGCCTACGCGGATGTTTCCGTGATCATTCTGGAAATCCTCATCGTGGTGATTG
 TCATTGAAGTAATCTCCAACGCACTTCGAAAGAGGCTGGT

>RXN01000
 ATGAGCACCTTAACCTCTACCGCACAGTACCGGCCCCCAGCTCTCCCCGGCGCGCCCC
 AACAACTGGCGCGCAATATCGTTGCAATTGTGCGTGCCTGATTGTCCTTATAGCTACC
 GGCACGCTCAAGATCGAGTGAATGAGCTTCCGCAGATGCCCGCGCAGGTGTGGCATTAC
 TTAGAGCTGATGTTTAGCGATCCCGATTGGTCTGAAGTTTGGCCGCGCCGTCCAGGAAATG
 TGGCGTTCCATCGCCATGGCGTGTTGGGTGCCATTTTATGCGTGTTGGTCTCTGTCCCT
 CTGGGAATGTTGGCTGCCCCGCGGGTGGGACCTTATTGGCTGCGTACCGTTTTACGGTTC
 GTGTTCCGCGTGATTTCGTGCGTTCCCCGAAGTGTTATCGCAATTATTTTGCTAACTGTC
 ACCGGCCTAACTCCTTTTACTGGTGCCTCGCATTTGGGTATCTCCGGTATTGGACAACAG
 GCAAAGTGGACCTATGAAGCCATTGAGTCCACTCCACCGGCCCCGTGAGAGGCAGTGCGT
 GCAGCGGTGGAACCTACGCCGAGGTTCTGCGGTGGGCGTTGTGGCCACAGGTTGCGCCA
 TCCATTGCATCTTTTGCCCTGTACCGCTTTGAGATCAACATCCGTACCTCTGCGGTATTG
 GGCATCGTTGGTGCAGGTGGTATCGGTAGTATGCTTGCCAATTACACCAACTACAGGCAG
 TGGGACACCGTGGGCATGCTGCTCATCGTCTGTTGTGCGCAACGATGATCGTCGATCTC
 ATCTCCGGCACCATCCGCCGCGCATCATGAAGGGGCTAGTGACCGTGTGTTGGCACCA
 AGCAAC

>RXN01000-downstream
 TGACGCTCCACCAAGCATCCGCA

>RXN01002-upstream
 GACTGCTGATACCGCACAGGATGAAATCACTCGTTACGGCGAGATCCTGAAGAAGTTCTC
 CAACATAATTTCCCTGTTTCCAATACTCAAGGTGTGCGCAT

>RXN01002
 ATGAATTCTGATGCTTCGGCTACCACCAACTCCTGGGCTATCAACTTCGACCATGTGTGCG
 GTGACGTATCCCAATGGGACGAAAGCCCTCGATGATGTTTCCCTCACCATCAATCCCGGT
 GAGATGGTTGCCATCGTGGGTCTGTGAGGATCGGGTAAATCCACGCTGATTCGCACGATC
 AACGGTCTTGTCCGCGCTACGGAAGGCACCGTGACGGTGGGGCCGCATCAGATCAACACC
 TTGAAGGGGAAAGCACTGCGTGATGCCCCGTGGGCAGATCGGCATGATTTTCCAGGGGTTT
 AACCTGTGCGAACGCAGCAGTGTGTTCCAGAATGTTTGGTGGGCGCTTCGCGCACACA
 CGCTGGTGGCGTAACCTCCTCGGGTTTCCACGGAGCACGACAAGCAGATTGCTTTTACAC
 GCGTTGGAGTCCGTGGGCATTTTGCACAAAGTGTGGACCCGAGCTGGTGCTTTGTGCGGT
 GGACAGAAACAGCGGTTGCTATTGCGCGCGCCTTATCGCAAGATCCGTCTGTCATGCTG

GCAGATGAGCCTGTGGCAAGCCTTGATCCGCCAACCGCGCATTCCGTGATGCGCGATCTA
GAAAACATCAACAACGTGGAAGGCCTCACCCTGTTGGTGAACCTGCACTTGATTGATTG
GCTCGTCAATACACCACAAGGCTTGTGGGTTTTCGTGCCGGCAAGCTGGTCTATGACGGT
CCTATCTCTGAGGCCACCGATAAAGACTTTGAAGCTATCTATGGTCGCCCCATCCAGGT
AAAGACCTGCTAGGTGATCGCGCA

>RXN01002-downstream
TGACCACGCCTTCTTCTACACTT

>RXN01141-upstream
AAAGAACACTCGGTATGGCACCTGATTTAAGGATGCTGCAATCGTGACACATATCCTCTT
CGACAGCAGGCGTTTTCTGCAACTGGGCGCTTTTTCGTCC

>RXN01141
TTGAGCACCGCATTGGCCGGAGCGGCCCCGCTACGTGACGTGCGACAAGCAATAATGAACCT
GCGGATAACACTCCCCTGACCATTGGCTACGTGCCTATTGCGGGCTCGGCGCCGATTGCT
ATCGCAGATGCGCTAGGGCTGTTTAAGAAACACGGCGTGAATGTCAGTTGAAGAAGTAC
TCAGGCTGGTCCGACCTGTGGACCGCCTATGCAACAGAGCAGCTTGATGTTGCGCACATG
CTGTCGCGCATGACTGTGGCGATTAAATGCTGGAGTGACCAACGCGTCGCGCCCGACGGAG
CTGTCGTTTACCCAGAACACCAATGGGCAAGCAATTACCTTGGCGTCAAAGCACTATGGT
TCCGTCAATTGACGCGCGGATCTTAAAGGCATGGTGTGGGAATTCCTTTTGAATATTCA
GTCCATGCGCTGCTCCTGCGCGATTATCTCGTCTCAAACGCAGTTGATCCCATCGCCGAT
CTTGAGCTTCGCCTGCTCCGACCTGCCGATATGGTTCGCACAATTGACAGTTGAGGGCATC
GATGGATTTCATTGGGCCTGGGCCGTTTAAATGAACGCGCCATCAGCAATGGCTCCGGCCGG
ATTTGGCTGCTGACCAAAACAACCTGTGGGACAAACATCCATGCTGCGCCGTGGCGATGGCC
AAAGAGTGAAAGCTGAACACCCCCACGGCGGCTCAGGGTGTGCTTAATGCGCTGGAGGAA
GCCTCCGCAATTTTGTAGCAATCCGGGCACAATTTGATTCTCGGCACGCACGCTGTGCGCAG
GAAAAATACCTCAACCAGCCTGCCACGTTGCTGGATGGACCGTCC

>RXN01141-downstream
TAATCATCGGCATCACCGGCTTA

>RXN01142-upstream
CTCCCCATCCACCGGCACAGTCAGCGCAGGCAACGAAGAAATTAAAGGACCAGGACCTGA
CCGAGGCATGGTTTTTCCAAGACCACGCCCTCCTGCCCTGA

>RXN01142
TTGACCGCACGCGGCAACATCGACTTCGGGCTCCGCTCCGCGCGCCCCCTCCTTGAGCAAA
ACCGAACGCGCCGACATCACCCGCACCCACCTCGAACAAGTAGGCCTCACCGACGCCGCC
GAACGGCGCCCCGCGCCCTCTCCGGCGGCATGCAACAGCGAGTCGGCATCGCACGCGCC
TTCGCCATCGACCCACCAATCATGCTTCTCGACGAACCCTTCGGCGCCCCCTCGACGCCCTC
ACCCGCCGCAACTCCAGCTCCAACTACTCAACATTTGGGAAGCCTCCCGCCGACCCGTC
GTCATGGTCAACCCACGACGTCGACGAGGCCATCCTGCTCTCCGACCGAGTTCTCGTGATG
TCCAAGAGCCCCGAAGCCACCATCATCACCGATATTCCAGTGAATCTTCCCCGCCCCAGA
CACGAGCTGAGTGAAGACGCTTCTGTTGAAGCCGAGACCACAGCCCTGCGTAAGCGGATG
CTGCATCTGCTGGAGCAC

>RXN01142-downstream
TAGTTTCTAACACGTCTTTTAAA

>RXN01164-upstream
GCCGATCGTGATTGATGAAGACGAGATCCAAGCCTGGACTTCTGATCTCAAACCTGAAGA
TTTACCAAAGGTAAAGATGAATCCGACGGTGAGAAATAA

>RXN01164
GTGACACTGTTTGTTCGGCTCGCCCTTGCTGCTGTGGGCGGGCTTTTTGTCTTTGCTTCC
AATGAACCGATCGGCTGGTTTGTGCGGGGAATTGTTGGCACTGCATTATTTTTATCTCC
CTTGCGCCGTGGGATCTGGGAGTTCCCCAAAAGCGCGGAAGAAGAATGAGCCAGTCCCCA
TTTTTGAACAGATGTCCACGGGCCCAACTGTTGTACAGGGCATGCTTTTAGGTTTTGTG
CATGGCCTGGTGACATATTTGCAGCTGTTGCCGTGGATCGGTGAGTTTGTGGCTCACTG
CCTTATGTCGCGTTGTGCTGAGGCGCTTTATTCCATTGCTCTTGGTGCTTTCGGC

GTGCTCATTGCGCGTTGGAGGGACTGGAAGGTTCTCCTGTTTCCGGCGATGTATGTGGCT
 GTGGAGTATCTAAGAAGCTCGTGGCCATTTGATGGATTTCGCGTGGGTTCGCCTGGCATGG
 GGTCAAATTAACGGTCCGTTGGCTAATCTCGCAGCGCTTGGTGGGGTAGCGTTTGTCACT
 TTTTCCACGGTGCTGGCTGCCGTGGGTGTGGCCATGGTGATTATTTCCAAGAAGCGACTG
 GCCGGCGCAATCATCACCGGAGTGTGATTGCTATCGGCGCGGTGTCATCCCTGTACGTT
 GACCGCAATGGCACGAGCGATGAAAGCATCGAAGTAGCCGCAATTCAGGGCAATGTGCCT
 CGGATGGGATTGGACTTCAATGCACAGCGCCGCGCGGTGCTGGCGAATCACGCACGGGAA
 ACCCTCAAGCTGGATGAACAAGTGGATTTGGTGATCTGGCCGGAGAATTCCTCAGACGTC
 AACCCATTTTCCGATGCACAAGCAAGAGCCATTATCGATGGAGCAGTGGAACATGTTTCA
 GCACCTATTTTGGTGGGCACGATCACCGTCGATGAGGTGGTCCACGCAACACCATGCAG
 GTATTTGATCCTGTTGAAGGTGCCGCGGAGTACCACAATAAGAAGTTCTTGCAGCCGTTT
 GGTGAATACATGCCGTTTCGCGAATTCCTGAGAATTTTCTCGCCCTACGTTGATTCCGCT
 GGAACTTCCAGCCCGGTGATGGCACCGGCGTAGTGGAGATGAATGCTGCGAACTTAGGC
 CGCGCTGTGACAGTGGGCGTGATGACGTGTTACGAGGTGATCTTGCACCGTGCTGGCCGC
 GACGCCATCGCCAATGGGGCTGAATTTTGGACACGCCACCAACAACGCCACCTTCGGA
 TTCACGGACATGACGTATCAGCAATTAGCAATGAGCAGGATGCGTGCCATCGAATTTGAT
 AGGGCGGTGGTTGTTGCAGCTACATCGGTTGTTTCGGCTATCGTCAACCCTGATGGAAGC
 ATTTCCAAAACACCCGAATTTTGGAGCCGCCACCTTGACGGAATCCATTCCACTCAAG
 GACACTGTCACCATCGCAGCGCGGGTTGGTTTCTATGTTGAATTACTGTTGGTTATCATT
 GGTGTATTAGCTGGACTATTCGCCATTCGAATGAATAGCCGTTCAAAGTCTGCGAAAGGT
 TCCGCTCGGCCCGCACAAGTTCGGGTTAAGAAGGTGCCTGCGAAAAAGGCAGCAACTAAT
 CGTCGAAAAGTAAAA

>RXN01164-downstream
 TAAAAACGTCCCGAAGGGACGAG

>RXN01168-upstream
 CCGCACAAAGTTTCGGGTTAAGAAGGTGCCTGCGAAAAAGGCAGCAACTAATCGTCGAAAAAG
 TAAAAATAAAAAACGTCCCGAAGGGACGAGGAGGACAACACC

>RXN01168
 ATGAGCAGTGAGGCAGTAGATGCTACGACGCTGGTGATTATTTCCAACGTACAACGAGCTG
 GAAAACCTTCCACTCATCGTGGATCGCGTGCGCACCGCAACCCCTGACGTTACGTAATC
 ATCGTGGACGACAACAGCCAGACGGCACCGGCGAGCGCGCAGACAAGCTTGCTGCTGAC
 GACGACCACATTTTGTCTCCACCGCGAAGGCAAAGGCGGCGCTGTGCGCAGAGTACATG
 GCTGGCTTCCAGTGGGGCTGGAGCGCGACTACCAGGTCTGTGCGAAATGGACGCCGAC
 GGCTCCACGCAACAGACGTGCACCTGCTGCTGCTGAGATACCAATGGCGCTGAC
 CTGGTCATCGGCTCGCGCTACGTGCCAGGCGGCGCGTAGTCAACTGGCCCCAAGAACCGT
 TGGCTCTTGTCGAAGGCGGCAACGTCTACATCAGCGTCGCGCTCGGCGCGGCTTGACC
 GATATGACCGCAGGTACCGCGCTTTTCGACGTGAAGTGCTAGAAGCACTGCCGCTTGAT
 GAGCTCTCCAACGCTGGGTACATTTTCCAAGTTGAGATTGCCTACCGTGCAATTGAAGCC
 GGATTGATGTTGTTGAAGTTCCCATCACTTTACCGAGCGTGAGATCGGCGAATCCAAG
 CTGGACGGCAGCTTTGTCAAGGATTCCTGCTCGAGGTAACCAAGTGGGGCTCAAGCAC
 CGCGGTGGCCAGGCCAAGGAAGTGTCCAAGGAAATGGTGGCGCTGCTGAAGTATGAGTGG
 AAGCACTTCAAAAAGCGCAACACCTGGCTC

>RXN01168-downstream
 TAAACTGCTTGCCGGTTAGTGAA

>RXN01285
 CTCAACGTACCATCCCCGACAACACCTTCACCGCCATCATCGGCCCCAACGGCTGCGGC
 AAATCCACCCTGCTCCGCGTTTCTCCGCGTGCTCAATCCGCAGCACGGCAAAGTGCTT
 CTCGACGGTGGCAACTCGATTCAATCAAGCCTAAAGAGATCGCCGAGAACTAGGCCTG
 CTGCCACAGACCTCCATCGCCCCAGAAGGCATCCGGGTTTACGATCTCATCGCGCGCGGG
 CGCGCTCCCTACCAAAGCCTCATACAACAATGGCGCACCTCCGACGAAGACGCCGTGCGG
 CAAGCGCTCGCCTCCACGAATCTCACCAGACTTGACGCTCGCCTCGTCGATGAAGTCTCC
 GGTGGCCAGCGCAACGAGTGTGGGTGGCCATGTTGCTCGCCAGCAAACACCGATCATG
 CTTCTCGACGAGCCACACCTTCCCTCGACATCGCCACCAATACGAAGTCTTGAATTG
 CTGCGCGCATTAACGAGGCGGGGAAAGTGTGGTCACTGTGCTTACGATCTCAACCAA
 GCCGCGCTACGCCGACCACCTCATCGTGATGAAAGATGGGCACGTACATGCCACGGGC

ACACCGGAGGAAGTCTTAACCTGCCGAGATGGTTCAAGGAGTTTTTGGCCTGCCCTGCATC
ATCTCCCCAGACCCCGTCACAGGAACCCCCACCGTCGTTCCCTCAGTCGGTCTCGCGCA
GGAGCT

>RXN01285-downstream
TAAGTAGCTACCCCTCCAACGGA

>RXN01298-upstream
CTTAAACGTACCTTATTTATGCATTATGTTGGTTTCAGACTCGAACAATTCAATTAGAA
AACACTAATCGGACATTTAGGTACATAACATTTCCGCTC

>RXN01298
GTGTCCACATTAATTTCTGAACCCGAGGTGGATAAGCTACGTAAACGTGCCAAGAGATCA
AGGCGGACAGAATGGTGGCTTGCCGCGCACTTCTTGCCCCAAACTTGCTTCTCTTGGCC
ATCTTTACGTATCGGCCACTGTTAGATAACTTCCGGTTGTCCTTTTTCAACTGGAACATT
TCCTCGCCACATCAACCTTCAATTGGGTTTGATAACTACGTTGAGTTCTTCACTCGTAGT
GACACTCTCCAAGTTGTTTTAAACACCGTCATCTTCACGGCATGTGCTGTGATCGGATCG
ATGGTGCTCGGTTTGCTCCTGGCCATGTTGTTGGATCAGAAGCTTTTCGGCCGTAACCTT
GTGCGTTCCATGGTGTGTTGCCCGTTTGTGATTTCCGGTGCTGCCATTGGTGTTGCTTTC
CAGTTCGTTTGTGACCCTAAATTTGGTTTGGTTTCAGGACTTGCTGGGACGCATCGGCCGT
GATTCGCCACAGTTCTACCAAACCCCTAACTGGGCATTGTTTCATGGTGACGTTCACTTTC
GTGTGGAAGAACTTGGGCTACTCCTTTGTTATCTACCTGGCTGCATTGCAGGGGCTAAAC
AAGGATTTGTCTGAGGCCGACCGGTGGATGGCGCGAGCGCTGGACACGTTTTTGGGAAG
GTTACTCTTCCGCAGCTTCGCCCAACCACGTTCTTCTTTCTATTACTGTACGCTGAAC
TCGGTTCAGGTCTTCGACATCATTCACACCATGACTCGTGGTGGCCCCCTTGGGTAACGGT
ACGACCACCTTGGTTTACCAGGTGTACACCGAGACTTTCACCAACTATCGCGCGGGATAT
GGTGCAACAATCGCAACGATTTTGTTCCTGTTGCTGCTGATTATCACTGTTATCCAGGTT
CGATACATGGATAAGGAGAACAAGCAGAAA

>RXN01298-downstream
TGATCTCGACTGATAGAAACGTT

>RXN01323-upstream
CACGTGGTTTACGCCAGGCATGTTCCCGCGAAGGGTTGACCCATACCCCTAGGGGGTATA
CAGTGAGTCATGTAAACATACTCGCAGAAGGAGCGATCCC

>RXN01323
ATGGCTCAGACACCCGCCAAAATCCCGCGGCACTGAATTTCAATTGACGTGACCTCGGC
GTTACCGGCATGACCTGCACCTTCTTGCTCCGCGCGCTCGAGCGCAAACCTGAACAAGCTC
GACGGCGTTGAAGCAACCGTCAACTACGCGACGGAATCCGCACAGGTCAGCTACGACCCC
TCAAAGGTCAGCCCTGAACAGCTGATTAAGACTGTTGAGGACACCGGCTACGGTGCTTTC
ACGATGGCTTCCGCAGCTGCCGAATCAGAAGAGGACAACGCTCCAGCTGACAGCGGCCAG
TCCCGCATCGACGCAGCTCGCGACCACGAAGCAGCCGACCTGAAACACCGCGTGATCGTC
TCTGCACTGTTGTGAGTTCCTGTGGTTTTGGTCAGCATGATCCCGGCGCTGCAATTC AAC
AACTGGCAGTGGGCCGTACTCACTTTGGTCACCCCGATTTTCTTCTGGGGCGGTTACCCG
TTCCACAAGGCAACGTGGGCAAACCTGAAGCGCGGTTCTTTCACCATGAACACCCCTGGTT
TCACTCGGCACGTCCGCTGCTGACCTGTGGTCCCTGTGGGCTTTGTTCAATTGAAAATGCT
GGTCACCCCTGGCATGAAGATGGAGATGCACCTGCTGCCGTGCGCCTCCACGATGGATGAG
ATTTACCTCGAAAACCGTCGCGGTGCTTATTACGTTCTGCTGCTTGGACGCTGGTTTTGAG
ACAAAAGCTAAGGGCCAATCTTCGGAAGCTCTGCGCAAGCTGCTGGACATGGGCGCCAAA
GATGCAGTCGTCTTACGTGACGGCGCCGAAGTCCGCGTTCTGTGAATCAGCTTAAACTC
GGCGACGTTTTTCATCACCCGCCCGCGGAGAAAATCGCCACCGACGGTGAAGTCGACGAA
GGTTCTCCGCGAGTCGACGAATCCATGCTCACCGGCGAATCCATCCCCGTTGAAGTCACC
AAGGGCTCCAAAAGTTACCGGCGCAACGCTGAACACTTCCGGCGCCTCATGGTGAAAAGTA
ACCCGCATCGGCGCCGACACCACCTGTGCGCAAATGGCTAAACTGGTCACGGACGCACAG
TCCAAAAAGTCCCCCTGTCCAGCGTCTTGTGACCAAATCTCGCAGGTTTTTGGTTCCCGTT
GTCAATCGTAATTGCTATTGCGACGCTGATCGCGCACCTCGTCTTCAACGACGCGCGCCTC
GCCCCAGCATTACCCGCGAGCAGTCGCGGTCTCATTATCGCCTGCCCTTGTGCCCTCGGC
CTGGCAACCCCAACCGCACTTCTGGTCGGAACCGGCGCGGCGCGCAACTTGGTCTGTTG
ATCAAGGGCCCTGAAATCCTCGAATCCACCAAAAAAGTCGACACCATCGTCTCTGACAAA

ACCGGCACCGTCACCACCGGCACCATGTCCGTCACCGACGTCACCGCCATCAACTACAGC
 GAAACCGAAATCCTCGAATTCGCTGCAGCCGTCGAGTCCGCCTCCGAACACCCCATCGCC
 CAGGCAATCGCCAAGGCCGCCGAACACGAGCAAGTCACCGACTTCCAAAACACCGCAGGT
 CAGGAAGTCACCGGTGTAGTCCGCGGACACGAGGTCCGCGTGGGCAGGCCCTTCAAGCACG
 CTTATCGACGCCCTCCTCCACCCCTTCCAACACGCCCCAAAAATCGGCGGAACCCCGTA
 GTCGTCACGATTGACGGCGTAGATTCCGGAATAATCACGGTCCGCGACACCGTCAAAGAC
 ACCTCCGCCGAAGCAATCCGCGGACTCAAGGAACTGGGACTCACCCCAATCCTACTCACC
 GGAGACAATGAAGGCGCAGCTAAATCCGTAGCCGCTGAAGTCGGCATCGACCAAGTCATC
 GCCAACGTCCTCCCCACGAAAAGTCCAAAACGTAGAAGCCCTCCAAGCACAAGGCAAA
 AACGTTGCGATGGTGGCGACGGCGTCAACGATGCCGCAGCTCTTGCCCAAGCTGACCTC
 GGAATCGCCATGGGAGCCGGCACCGACGTAGCCATCGAAGCCTCCGACATCACCCTCATG
 AACAACGACCTCCGATCCGCGAGTCGACGCCATCCGACTGTCCCGTAAAACCCCTCGGCACC
 ATCAAGGGAAACCTTTTCTGGGCTTTCGCCTACAATGTTGCACTAATCCAGTAGCGGCG
 ATCGGACTCCTCAACCAATGCTTGGCGGCATTGCGATGGCCTTCAGTTCAGTTTTCGTC
 GTCTCCAATTCCTTGGCTCTGCGAGGATTCAAAGCAAGGAGCAAC

>RXN01323-downstream
 TAATGTCCAACAGCGAATGCCAC

>RXN01338
 AAAACTTATACCCCAAATCCCTGGATGTTATTCATCCGCTCATTTGATGGCATCATCACT
 GTCGCAGCCCTTGTGGCATCGCAATACATCTCATTTTATGGCTGGCTCTAGATCTAGAT
 GGCCTTGCTAAAACTGGCCTTTAATAGCCATCGTTATCGTAGGTGGCATTCGGTTGATG
 TGGGATGTGCTGAAATCAGCCATTAAAACCTCGCGGTGGCGCGGATACTTTAGCAGCAGTC
 TCCATCATTACTTCTGTGTTGTTAGGGGAGTGGTTGGTTGCCGCGATCATCGTGCTCATG
 CTCTCTGGTGGTGAAGCGCTAGAAGAGGCAGCATCACGGCGAGCCAGTGGCACCTTGGAC
 GCACTTGCCCGGCGCGCACCAAGTACAGCTCACCGCCTGTTGGGTGCAACCATTCTTGAT
 GGAACCGAAGAGATCGCCGTGGAAGAGATCACGGTTGGTGATTTAGTGGCGGTGCTCCCG
 CATGAACCTTTGTCCCGTGGATGGTGAATCGTGGCAGGCCACGGCACCATGGATGAGTCT
 TATCTCACGGGTGAGCCCTATGTGGTGAGTAAATCTAAAGGTTGCAAGCAATGTCGGGT
 GCAGTCAATGGTGATACTCCGCTGACGATTGTTGCCACAAAGCTTGCCCATGATTCCAGA
 TACGCCCAAATTTGTTGGTGACTCCATGAAGCAGAAAACAACCGCCCAAGAAATGCGCAGG
 ATGGCTGACCGTCTTGGCGCGTGGTATACGGTGATTGCACTTGCCCTCGGTGGTCTTGGC
 TGGATTGTCTCCGGCGACCCAGTGAGGTTCTTGGCTGTTGTGCTTGTGCGCCACCCCATGT
 CCATTGCTCATTGCACTGCCAGTGGCGATCATCGGTGCGATTTCTCTTGGCGCTCGTCCG
 GGCATCATCGTGAAGAACCCTGGAATGCTGGAAAACGCTTCAGGAGTAAAGACAGTGATG
 TTCGATAAGACTGGAACGCTCACCTATGGCAGGCCAGTGATTACTGATATCCACACTGCT
 CCCGGAGTTGAGGAAGATACAGTCTTAGCTTTGGCTGCTTCAGTAGAGCGCTACTCCAGA
 CACCCGTTGGCTGACGCGATTTCGTGAGGGCGCAAAGCCAGGGAACCTTCATCTGCCTGAT
 GTAGTGAAGTATCGAACGTCACAGGACAGGACTAACCGGCACGGTGGGCGAGCACCTG
 GTTCGAATAACCAATAGGCGCAGCACACTAGAAATTGATCCAGACAGCAAGAACTACATT
 CCGGTGACAAGTTCCGGCATGGAATCTGTGGTGCTTGTGATGATAAATATGCAGCACTC
 ATTCGCCTCCGGGATGAACCTCGTGCATCTGCCAGTGAGTTCATCGCGCACTTGCCCAAG
 AAGCACAAAGTGACAAGCTCATGATTATCTCTGGTGATCGCGCATCTGAGGTTTCGTTAC
 CTTGCGGACAAGGTTGGCATTGATGAGGTACACGCAGAGGCCTCACCGGAAGACAAGCTG
 AACATTGTTAATCGGCATAATGAGCACGGCGCCACCATGTTCTTAGGTGATGGAATCAAC
 GATGCGCCAGCCATGGCCGTTGCCACCGTTGGTGTCGCGATGGGAGCAGACTCCGATGTC
 ACGTCCGAAGCAGCAGATGCTGTGATTTTGGATTCTTCCCTGGAACGTCTCGACGATCTG
 CTCACATCAGTGCACGGATGCGTGAATAGCGTTGCAATCTGCGGGCGGTGGCATGGCG
 TTGAGTGTCATAGGAATGATCCTCGCGGTATTTGGATTCTTGACGCCACTGATGGGTGCG
 ATCTTCCAAGAGGTCATTGACGTGCTGGCTATCCTCAATTCCGCTCGGGTCGCACTGCCA
 CGCGGAGCGATTAGTGATTTTGATACGCAAGAAAAAGTTTCT

>RXN01338-downstream
 TAGCAGGGTAACCTAAATGTCGT

>RXN01411-upstream
 CTTATCGACGTCCCCATCCCCCTCGCCAATGCTTCGGCGAGGGTTCTATTTATTGTGTG
 TGCTAGCCTTTTCGCAATCGTTCAGCCCCGCCCGACGTCA

>RXN01411

ATGTTGGGAGTGGGCTGGCGCATTCCATTCTGATGGCCGTGCCACTAGGGCTTATCGGC
 TGGTGGATCCGCACCGGTGCCAGGAAATGTACGCCCCGCATCCGAACGCCCCGAAGCT
 CCTATTAAGCAGGCATTGCGTACTGAGTGAAGATGATGTTGCGGGTAGGTGGCTTTATC
 TCTTGCACCGGTCTGAGCTTCTACATTTTACCACGTACATGACCACTTTCTTGCAGC
 ACCGTCGGACTGGAGGGCACGTTAGTGTCTGGCTGGAAACATCATCGCTCTCAGCATGGCA
 GCAATTGTGGCCCCATTGTTGGCCGCGCAATTGATAAATTCCCCCGCCGGAACATCATG
 GCTTTCGCTACCTTAAGCACAGTAATTATGGCGATCCCGGCCTACATCATTGCAGGTCAA
 GGTACTTTGACTGCTTCTTTGATTGCGCAGGTAATGCTTGGAATCGGCGCGGTTACCGCT
 AACTGCGTTACCTCAGTAATGATGGCCGAGGTCTTCCAAGAGGTCAACCCGCGGTACTTCC
 GCCGGCATTACCTACAACGTCACTTACGCAATCTTCGGCGGCTCGGCTCCATTTATCTCC
 ACCGCATTGGTCTCTGACCGGCGAGCCCGCTGGCCCTGCGGTATACATGATCATCATT
 GCGCTCTTCGCCTTACCGCGTCCCGCTTCATTCTGAAACCTCCCCAGTTTTTGTCCAC
 GCAACCCCGGCCATTAAGGCACCAAAGGTGCTGGTCAACCCGGGT

>RXN01411-downstream
 TAAACCACGCTTTTCGACGAAAA

>RXN01808
 CAGAGCTCGCGTGTAAGAAGTTCGCATGGATGCGCGGCGGTGCACCAGCGCGAACCTCA
 AAGCCTGGATTCCGCCTTGAAGCCGCGGAAGCTTTGATCGCAGAAAGTGCCAGCGCCACGC
 GACAAAGTCGAGCTCATGGCATTTCCTCAAGTCCAGGCAAGGCCGCGTTGTCATTGAACTT
 GAAGACGCCACAGTAGCCACCCCTGATGATCGCATCTTGGTAGAAGACCTCACCTGGCGT
 TTGGCTCCAGGAGAGCGCATCGGTCTTGTGGCGTCAACGGCTCCGGCAAAACACCCCTG
 CTGCGCACCCCTTGCCGGCGAGCAGCCACTTCAGGCAGGCAACGCATCGAAGGCCAAACC
 GTCAAACTGGGATGGCTCCGCCAGGAACTCGATGACCTAGACCTCAGCCGCCGACTCATC
 GACTGCGTTGAAGATGTCGCTTCTACGTGATGATGGGCGACAAGCAGGTCTCCGCTTCC
 CAATTGGCAGAACGCTCGGATTCTCACCCAAGAGGCAACGCACCCCAAGTTGGTGACCTG
 TCCGGTGGTGAACGCCGCCGACTCCAACCTACCCGCGTGCTCATGGCCGAACCAACGTG
 CTGCTCCTCGACGAGCCACCAACGACCTGGACATTGACACCCCTCCAAGAGCTGGAATCC
 CTTCTCGACGGATGGCCAGGCACCATGGTGGTTATCTCCACGACCGTTACCTCATCGAA
 CGCGTCACCGACTCCACCTGGGCACTCTTCGGCGATGGCAAGCTCACCAACCTGCCAGGC
 GGAATTGAAGAGTACCTGCAGCGACGAGCAGCATGGCCGCGCCGAAGACAGTGGAGTG
 CTGAACCTTGGGTGCGGCCACGCAGGCTGGAACCTTTTCTGCTGCAACAGAGCAGGCTGCC
 ACTTCTGTGGAAGTTCCGGAATTTCTTCCCAAGAAGCCACCGCATCACCAAGGAAATG
 AACGCCCTGGAGCGCAAAATGGGCAAGCTTGACCAGCAAATGGACAAGCTTAATCAGCAG
 CTCGCTGATGCAGCGGAGGCCATGGACACCATAAAGCTCACCGAGCTGGACACCAAGCTC
 CGCGCAGTGCAGGAAGAACACGGCGAGCTGGAATGCAGTGGCTGGAACCTCGGCGAGGAA
 ATCGAGGGC

>RXN01808-downstream
 TAGTTCATGCCGTGCGCAGGCGA

>RXN01939-upstream
 TGCTGTTCTACCCCGCAATGGCACATTGCACTAACCGTTTTGAGCTTCATCATGATGGCG
 ATGTCTGCCGCGACGCTCTGGATCCTAAGTCGAGGAAGCG

>RXN01939
 ATGACCACCAACATCCCACAAACCCCAACCACGAGGGTGAACAGCCACTGCTCGAGCTG
 AAGGATCTAAAGATTTCTTACCTCCTCCACCGGTGTTGTCGACGCTGTCCGTGGCGCA
 AACCTCACCATTTATCCTGGCCAATCTGTTGCCATCGTGGGTGAATCCGGTTTCAAGTAAA
 TCGACCACGGCAATGTCGATCATCGGTCTGCTTCCAGGCACCGGCAAGTGACCGAAGGT
 TCCATCATGTTTGTATGGCCAAGACATCACAGGCTTGAGTAACAAGCAGATGGAAAAGTAC
 CGCGGTTTCAAAATCGGACTGGTCCCCAGGATCCGATGACCAACTTGAACCCGGTGTGG
 CGCATCGGCACCCAGGTCAAGGAATCCCTCCGAGCCAACCACGTGGTTCCAGGCTCAGAG
 ATGGACAAGCGCGTGGCAGAAGTTCTGGCCGAGGCAGGTCTTCTGATGCTGAGCGTCGC
 GCAAAGCAGTACCCACATGAGTTCTTGGCGGTATGCGCCAGCGCGCACTGATCGCCATT
 GGTTTGGCGGCACGCCGAAGCTCTTGATCGCCGACGAGCCACCTCTGCGCTGGATGTC
 ACCGTGCAGCGCAAAATCCTTGATCACCTTGAAACACTGACCAAGGATCTCGGCACCGCA
 GTGCTATTTATTACCCACGACTTGGGCTTGGCGCTGAGCGCGCGGAGCACCTCGTGGTG
 ATGCACCGCGGACGCATCGTGGAGTCCGGGCCATCATTGAAGATTCTGCGCAATCCACAG
 CACCCATATACCCAACGCTTGGTTAAGGCTGCGCCGTCTCTGGCTTCTGCACGTATTCAA

AGTGCGCAGGAACAAGGCATTGAATCTGCAGAACTGCTCTCTGCAACGGCCGTTGCTGAG
GGCACTATTCCAGAGATGGAAGAAAAAGTTATCGAGGTGAAAAACCTCACCCGCGAATTT
GATATCCGCGGTGCCCGTGGCGATAAGAAGAAGCTGAAGGCCGTTGATGATGTGTCCTTC
TTCGTACGTAAAGGCACCACCACCGCACTTGTGGGTGAATCCGGTTCGGGTAAATCCACC
GTGGCCAAACATGGTGTCAACCTTCTCGAGCCAACCAGCGGAGAGGTGCTCTACAACGGC
ACCGATCTTACGTCTTGTAGCCACAAGGAAATCTTCCAAATGCGACGCAAACTGCAGGTG
GTGTTCCAGAACCCCTACGGCTCGCTTGATCCGATGTACTCCATCTACCGGTGTATTGAG
GAACCGCTGACCATCCACAAGGTTGGTGGAGACCGCAAGGCACGCGAAGCTCGCGTCGCT
GAACTTCTCGATATGGTGTCCATGCCAGGTCCACCATGCGCCGCTACCCCAACGAGCTT
TCCGGTGGCCAAACGTACGCGCATCGCCATCGCCCGTGCATTGGCACTGAATCCAGAAGTG
ATCGTGTGGATGAAGCGGTTTCCGCTTTGGACGTGTTGGTTCAGAACCCAGATCCTCACC
CTGCTTGCAGAACTTCAGCAGGAACTGAAGCTCACCTATTTGTTTCATCACCCACGACTTG
GCCGTTGTTTCGACAAACCGCCGACGATGTTGTGGTGTATGCAAAAGGGACGAATCGTTGAA
AAGGGTCGTACCGACGACATCTTCAACGATCCTCAGCAGCACTACACCCGCGATTGATC
AATGCGGTACCTGGTCTGGGAATCGAGTTGGGTACTGGAGAAAACCTGGTT

>RXN01939-downstream
TAACCCGCACAGCCTCACTAAAC

>RXN01995-upstream
CCGACGCAAAGGCATGCGCTGCGTGTCTCGAGTAGTCTCCTCCCCTTCCTCGTCCCCAA
CCTCGACCATTACGGTCGCCCTCTCCTAAAGGAGCCTGGC

>RXN01995
ATGGATATCCGCCAAACAATTAACGACACAGCAATGTCGAGATATCAGTGGTTCATTGTA
TTTATCGCAGTGCTGTCAACGCACTGGACGGCTTTGATGTCTCGCCATGTCTTTTACT
GCGAATGCAGTGACCGAAGAATTTGGACTGAGTGGCAGCCAGCTTGGTGTGCTGCTGAGT
TCCGCGCTGTTTCGGCATGACCGCTGGATCTTTGCTGTTTCGGTCCGATCGGTGACCGTTTC
GGCCGTAAGAATGCCCTGATGATCGCGCTGCTGTTCAACGTGGTGGGATTGGTATTGTCC
GCCACCGCGCAGTCCGCGAGGCCAGTTGGGCGTGTGGCGTTTGATCACTGGTATCGGCATC
GGCGGAATCCTCGCTGCATCACAGTGGTGTATCAGTGAATCTCCAACAACAAAAACCGC
GGCATGGCCATGTCCATCTACGCTGCTGGTTACGGCATCGGCGCGTCTTTGGGCGGTTTC
GGCGCAGCGCAGCTCATCCCAACATTTGGATGGCGCTCCGTGTTTCGACGCCGTGCGATC
GCAACTGGTATCGCCACCATCGCTACTTTCTTCTTCTGCGAGAATCCGTTGATTGGCTG
AGCACTCGCGGCCCTGCGGGCGCTCGCGACAAGATCAATTACATTGCGCGCCGCTGGGC
AAAGTCGGTACCTTTGAGCTTCCAGGCGAACAAGCTTGTGACGAAAAAGCCGGTCTC
CAATCGTATGCAGTGCTCGTTAACAAAGAGAACCGTGGAACCAGCATCAAGCTGTGGGTT
GCGTTCCGCATCGTGATGTTTCGGCTTCTACTTCGCCAACACTTGGACCCGAAGCTGCTC
GTGGAACCCGGAATGTGAGAACAGCAGGGCATCATCGGTGGTTTGATGTTGTCCATGGGT
GGAGCATTCGGCTCCCTGCTCTACGTTTCTCACCACCAAGTTCAGTCCCGAAACACA
CTGATGACCTTCATGGTGCTGTCCGGCCTGACGCTGATCCTGTTTCTTCTCCACCTCT
GTTCCATCCATCGCGTTTGGCAGCGGCGTTGTCGTGGGCATGCTGATCAATGGTTGTGTG
GCTGGTCTGTACACCTGTCCCCACAGCTGTACTCCGCTGAAGTACGCACCACTGGTGTG
GGCGCTGCGATTGGTATGGGTGCTGTGCGGTGCGATTTCCGCGCCACTGCTGGTGGGTGGC
CTGCTGGATTCTGGCTGGTCCCCAACGCAGCTGTATGTTGGTGTGGCAGTGATTGTTATT
GCCGGTGCAACCGCATTTGATTGGGATGCGCACTCAGGCGGTAGCCGTCGAAAAGCAGCCT
GAAGCCCTAGCGACCAA

>RXN01995-downstream
TAGGGCCGCGATTCTAGCATGC

>RXN02062-upstream
TTGTCTAAACATCGTTTTGGGGTCCGAATGATAGCCCCTTTTAATGCCCCATTTTCGGTA
TCGCTGCGCACTGTTTTTAGATGGCTAATCTTTGAAAT

>RXN02062
ATGAGAGTCCGAATGATGACAAGAGAGTATCCACCAGAGGTTTACGGCGGCGCTGGCGTG
CACGTACCCGAATTGACCGATTGATGCGTGAGATCGCTGAAGTTGATGTTCACTGCATG
GGTGACCTCGCGATATGGAGGGAGTTTTTCGTCCACGGCGTCGATCCTGCCTTGGAAAGC
GCCAACCCTGCGATTAAGACACTGTCCACCGGTTTACGCATGGCAGAAGCTGCAACAAC
GTGGATGTCGTGCACTCACACACTTGGTATGCAGGTCTTGGCGGCCACCTTGCAGCTCGT

CTCCACGGCATTCTCCTACGTGGCTACCGCGCACTCTTTGGAGCCAGATCGCCCATGGAAG
 CGTGAGCAGCTTGGCGGTGGATACGACGTGTCTCCTGGTCTGAAAAAATGCCATGGAA
 TACGCTGACGCGGTATCGCTGTGTGGCTCGCATGAAAGATTCCATCCTCGCTGCGTAC
 CCTCGCATCGAGCCGGACAACGTGCGTGTGTCTCAACGGCATCGACACTGAGTTGTGG
 CAGCCTCGCCCCGACTTTTCGATGACGCGGAAGATTCCGTACTCCGCTCCCTAGGCGTTGAC
 CCACAGCGGGCCATCGTTCGATTTGTGCGGCCGATCACCCGCCAAAAAGGCGTCGAGCAC
 CTCATCAAGGCAGCAGCGCTTTTCGACGAGTCCGTGCAGCTTGTGCTCTGTGCCGGCGCG
 CCAGACACCCCGAAATCGCAGCTCGCACCACCGCCCTGGTGGAAAGAACTCCAGGCAAAG
 CGCGAAGGCATTTTCTGGGTTTCAGGACATGCTGGGCAAGGACAAAATCCAAGAGATTCTC
 ACCGCTGCTGACACCTTCGTGTGCCCATCCATTTACGAGCCACTGGGCATCGTGAACCTTG
 GAAGCAATGGCCTGCAACACCGCAGTTGTTCGATCCGACGTTGGAGGCATCCCTGAGGTT
 GTTGTGACGGCACCACCGGCGCCCTCGTTTACTACGACGAAAATGATGTCGAAACCTTC
 GAGCGCGATATCGCCGAAGCGGTGAATAAAATGGTCGCTGATCGAGAGACCGCAGCCAAA
 TTTGGTCTCGCAGGGCGCGAACGTGCTATCAATGATTTCCTGGGCAACGATTGCTCAG
 CAGACCATTGATGTGTACAAATCCTTGATG

>RXN02062-downstream
 TAAAACCGAAAGCCGGGGAACCT

>RXN02096-upstream
 CGCTTCGACGACCTACCCACAGCGATATCCGCAGGAATCTCATCGCGTTTTTGTATGAG
 CCGTTCTTGATCTCTCCTCCATACCGCGAGAACATCTCG

>RXN02096
 ATGGGTTTGGATGTGATGATGAGCAGATCGAACACGCAGCCAGGCTTGCCCAGGCTCAT
 GATTTTATCGATCGCCTTCCAAACAAATACGAGGAAGTCATTGGCGAACGCGGCCTGACG
 CTTTCTGGTGGTCAACGCCAACGCATCGCCCTCGCACGGGCTTTCCTGGCGCATCCCAA
 GTGTTGGTGTCTGATGATGCCACCTCTGCCATTGATGCCTCCACTGAGGACCGCATTTTC
 CAGGCCCTTGCGCGAAGAACTGCACGATGTACCATTTTGTATCATCGCGCACCGCCACTCC
 ACTTTGGAGCTCGGCGATCGGGTTGGTCTGGTTCGAAGATGGACGGGTAACAGCACTGGGA
 CCGTTGAGTGAGATGCGTGATCACGCTCGTTTCTCGCATCTGATGGCTCTTGATTTCCAG
 GATTCTCACGATCCGGAATTACCCCTCGACAACGGTTCACTACCCAGCCAAGAGCAATTG
 TGGCCGGAGGTCTCCACAGAAAAGCAGTACAAGATTCTTGCGCCTGCCCCGTGGTCGAGGC
 CGTGGCATGTCCATGCCAGCAACCCCTGAGCTGCTCGCCAGATTGAGGCGCTGCCAGCA
 GCAACGGAAGAAACACGAGTTGATGCCGGGAGGCTACGCACCAGTACCTCCGTTTTCAA
 TTGCTCAGTTTATTCAAGCAGGTCCGTTGGCTCGTTCGTCGCGGTCATCGCGTTGTTGCTG
 GTGGGCGTAGCCGCCGATCTAGCATTTCCAACACTGATGCGCGCAGCCATCGACAACGGT
 GTGCAAGCACAAAGCACCTCCACGTTGTGGTGGATCGCCATCGCAGGCAGCGTAGTAGTC
 CTTCTGTCTCTGGGCCGCGCCGCGATCAACACGATTATCACGGCACGCACCGGTGAACGG
 CTGCTTTTACGGCTTGCGTCTGCGCTCATTTGTGCATCTATTGCGCCTGTCCATGAGCTAT
 TTCGAACGCACCATGTCCGGCCGCATCATGACGCGCATGACCACCGACATCGACAACCTC
 TCGTCTCTTCTCCAATCAGGTCTGGCGCAAACAGTTGTCTCTGTGGGCACGCTCATCGGT
 GTGGTCACCATGCTCGCCATCACCGACGCACAACACTAGCACTCGTTGCGCTGTCCGTGGTG
 CCGATCATCATCGTGCTCACTCTCATTTTCCGACGCATCAGCTCCAGGCTGTACACCGCT
 TCACGCGAGCAAGCCAGCCAGGTCAACGCGGTATTCCACGAGTCCATCGCCGGTTTACGC
 ACCGCGCAGATGCACCGCATGGAAGACCAAGTCTTTGACAATTATGCGGGCGAAGCAGAG
 GAATTCGACGCCTGCGTGTGAAATCCCAGACGGCCATCGCCATCTACTTCCCCGGCCTT
 GGCGCGCTCTCTGAAATCGCCAGGCACCTCGTCTCGGTTTCGGCGCACTGCAAGTAACG
 CGCGGCGACATCTCCACCGGCGTACTCGTGGCATTCGTGCTGTACATGGGCGCTGATGTTT
 GGCCCCATCCAACAATAAGCCAAATCTTCGACTCCTACCAACAAGCCGCGCTCGGCTTC
 CGTCGCATCACCGAACTGCTCGCAACGCAGCCAGCGTCCAGATCTGGGCACCAACAGGC
 ACGCTAGGCAGGCTGCCACGCAGCCTTTATTGCTTGACGACGTACCTTCGGCTATTTCAG
 ACGATCCGATCC

>RXN02096-downstream
 TAGACAACGTACCGTCCAGATC

>RXN02348-upstream
 AAAGACCCGAGCCGAAGCCCTGGCCTGCGCATACTTCTTGTCAACGCTCGCTGGGATTA
 GGTCTTTTCTGAGCGCTAGCATTTCTCCACTCAAAGGAGC

>RXN02348

ATGCTTAACCGCATGAAAAGTGCGCGGCCAAAATCAGTCGCTCCAAAATCCGGACAAGCT
TTACTCACTCTCGGTGCCCTAGGTGTTGTGTTTCGGCGACATCGGCACCAGCCCCCTGTAC
TCACCTCACACTGCATTTCAGCATGCAGCACAACAAAGTCGAAGTCACTCAGGAAAAATGTG
TACGGCATCATCTCCATGGTGTGTTGGGACCATCACTTTGATCGTCACCGTCAAATACGTC
ATGCTGGTCACCCGAGCTGACAACCAAGGACAAGGTGGCATCCTGGCGCTCGTTGCTTTG
CTGAAAAACCGTGGGCACTGGGAAAAATTTCGTGGCAGTAGCCGGCATGTTGGGCGCCGCA
TTGTTTTATGGCGATGTGGTGATCACCCCGGCGATCTCTGTTCTCAGCGCAACAGAAGGC
TTGACGGTTATCTCCCCAAGCTTTGAGCGCTTCATTCTGCCCGTATCTCTCGCAGTTCTG
ATCGCTATTTTTGCAATCCAACCGCTCGGTACAGAAAAAGTCGGCAAAGCCTTCGGCCCC
ATCATGTTGCTGTGGTTTGTACCCCTTGCAAGATTGGGAATTCGGCAAATCATCGGGCAC
CCAGAAATCTTCAGAGCTTGTCTCCACATTGGGCCCCGCGCTTGATTGTGGCTGAGCCT
TTCCAAGCATTTGTGCTGCTTGGTGCCGTTGTCTGACAGTAACGGGTGCGGAAGCGCTC
TACGCTGATATGGGCCATTTTGGGGCGAGGCCAATCAGAGTGGCGTGGTTTTGCGTCGTC
ATGCCTGCTTTAATCTTGACGATTTTGGGGCAGGGCGCCTTGGTGATCAACCAGCCTGAA
GCGGTGCGCAACCCCATGTTTTATCTCGCGCCGGAAGGTCTGCGGATTCCGTTGGTTATT
TTGGCGACCATCGCTACGGTGATCGCATCGCAGGCCGTGATTTCTGGTGCGTATTTCATTG
ACCAAGCAGGCCGTGAATTTGAAACTGCTGCCACGCATGGTGATCCGGCATACCTCCCGC
AAAGAGGAAGGCCAGATCTATATGCCACTGGTTAATGGATTGCTGTTGTATCCGTGATG
GTTGTGGTGCTGGTATTCCGATCCTCTGAAAGCCTCGCCAGCGCGTACGGACTTGCAAGT
ACCGGAACCTTGGTGCTGGTCAGCGTCTGTATCTGATCTATGTTACACCACATGGTGG
AAAACAGCGCTGTTTCATTGTGCTCATCGGTATTCCAGAAGTACTTCTATTTCGCCCTCGAAC
ACCACGAAAATTCACGACGGTGGCTGGCTTCCACTACTTATTGCGGCCGTGCTCATCGTG
GTGATGCGGACCTGGGAGTGGGGAAGTGACCGCGTCAATCAGGAACGCGCAGAGCTGGAA
CTTCCCATGGATAAGTTCTTGGAGAACTCGATCAGCCACACAATATTGGTCTGCGTAAA
GTTGCCGAAGTGGCAGTATTTCCACATGGCACCAGCGATACTGTCCCGTTGTCATTGGTT
CGCTGCGTGAAAGACCTCAAGCTTTTATACCGAGAGATCGTGATCGTTCGAATCGTCCAA
GAACACGTTCCGCACGTGCCACCAGAGGAACGCGCGGAAATGGAAGTGCTCCATCACGCC
CCGATCAGAGTCGTGCGAGTTGATCTGCACCTTGGTTATTTTGATGAGCAGAACCTGCCT
GAGCATCTCCATGCCATTGACCAACATGGGATAACGCCACCTACTTCTGTCTGCCCTG
ACTCTTCGGAGCAGGTGCTGCGAAAGATTGCTGGCTGGCTGATCGTTGTATCTTTTCG
ATGGAACGTAATCAGGCATCTCGAAGTGAAGTCTTTCAAATTGCAACCAAGCAAAACCATC
ACGGTTGGAACAGAGCTGCACCTT

>RXN02348-downstream

TAATCAGGCAGTTGCTGGCCAAC

>RXN02354-upstream

GAATAAAGAAAAAGAACTGGGCGGAACCAAGGATGAGAAACCCACCGCTAAGGATGCTG
TTGTAAAGGCCGATTCTGCTGTGAAGGAAGCCGCTAAGCC

>RXN02354

ATGACTAAACGAACAAAAGGACTCATCCTCAACTACGCCGGAGTGGTGTTTCATCCTCTTC
TGGGGACTAGCTCCCTTCTACTGGATGGTTATCACCGCACTGCGCGATTCCAAGCACACC
TTTGACACCACCCCATGGCCAACGCACGTACCTTGGATAACTTCCGGGACGCACTGGCC
ACCGACAAAGGCAACAACTTCTCGCAGCCATTGGCAACTCACTGGTCATCAGCGTCACC
ACAACAGCGATCGCTGTTCTCGTGGGAGTGTTACCGCCTACGCTCTAGCCCGACTGGAA
TTCCCGGGCAAAGGCATTGTACCCGGCATCATCTTGGCAGCCTCCATGTTCCCGGCATC
GCCCTGGTCACTCCGCTGTTCCAGCTCTTCGGTGACCTCAACTGGATCGGCACCTACCAA
GCGCTGATTATCCCGAACATTTCTTCGCGCTACCTCTGACGATCTACACGCTCGTATCC
TTCTTCAGGCAACTGCCCTGGGAACCTCGAAGAATCAGCACGTGTGACGCGGCCACACGT
GGCCAAGCCTTCCGCATGATCCTGCTTCTCTAGCAGCGCCCGCACTATTTACCACCGCG
ATCCTCGCATTTCATTGCAACGTGGAACGAATTTCATGCTGGCCCGCAACTATCCAACACC
TCCACAGAGCCAGTGACCGTTGCGATCGCAAGGTTACCGGACCAAGCTCCTTCGAATAC
CCCTACGCCTCTGTGATGGCAGCGGGAGCTTTGGTGACCATCCCACTGATCATCATGGTT
CTCATCTTCCAACGCCGCATCGTCTCCGGACTCACCGCAGGTGGCGTGAAAGCC

>RXN02354-downstream

TAGACTAGATACTCATGAGTGCT

>RXN02356-upstream

TTGGCAGTAGCCATGCGTTCTGCTCCTGACCTTGAACAGCGGTCCCAATTTAGACCCGCT
AAACCCACAATGTGTACTGGTGTGTAATTTAGTAGAAC

>RXN02356

ATGGCAACGGTCACATTCGACAAGGTCACAATCCGGTACCCCGGCGCGGAGCGCGCAACA
GTTTCATGAGCTTGATTTAGATATCGCTGATGGCGAGTTTTTGGTGCTCGTCGGCCCTTCG
GGTTGTGGTAAATCCACTACGCTGCGTGCTTTGGCGGGGCTTGAGGGCGTGGAGTCGGGT
GTGATCAAAATTGATGGCAAGGATGTCACTGGTCAGGAGCCGGCGGATCGCGATATCGCG
ATGGTGTTCCAGAATTATGCTCTGTACCCTCACATGACGGTGGCGAAGAATATGGGTTTT
GCGCTGAAGTTGGCTAAGCTGCCGACGGCGCAGATCGATGCGAAGGTCAATGAGGCTGCG
GAAATTCCTTGGGTTGACGGAGTTTTTGGATCGCAAGCCTAAGGATTTATCGGGTGGTCAG
CGTCAGCGTGTGGCGATGGGTGCGCGCTTGGTGCGTGATCCGAAGGTGTTCCCTCATGGAT
GAGCCGCTGTCCAACCTGGATGCGAAATTGCGCGTGCAAACCCGCGCGGAGGTGCGTGCT
TTGCAGCGTCGCTGGGCACCACCACGGTGTATGTACCCACGATCAGGTTGAGGCAATG
ACGATGGGCGATCGGGTTGCGGTGCTCAAGGACGGGTGCTGACGAGGTGCGACCGCCC
AGGGAGCTTTACGACGCCCGGTCAACGAATTCGTTGCGGGCTTCATCGGCTCGCCGCTC
ATGAACCTCTCCCTGCCAACGGGCACAAGATGGGTGTGCGCCCGGAGAAGATGCTGGTC
AATGAGACCCCTGAGGTTTTACAAGCATTGATGCTGTGGTGGATATCGTCGAGGAGCTT
GGCTCCGAATCGTATGTTTATGCCACTTGGGAGGGCCACCGCTGGTGGCCCGTTGGGTG
GAAGGCCCCGTGCCAGCCCCCTGGCAGCCTGTGACTTTTTCTATGATGCGGCGCAGGCG
CATCATTTGATCTGGAGTCGGGCGAGCGTATCGCT

>RXN02356-downstream
TAGTTTCGGACGTGGGGAGGCGT

>RXN02391-upstream

CAAAGTGGCGATCCTGAATTTGCCATCGAATCTGCCGTGAGAAGAGTTGCAGAGCTGGCG
AGGCGGTAACGCTGAACGGCGCGGGTAAGATATTTGAGC

>RXN02391

ATGACACAATCAGATTTACCCGATGATGTTTCAAGGAATTGGTCACTAAGATCTTTGGACTG
GCACGTGATGGGGGAGCAGAATCCGCAGCAACCCTCGGTGCATATGTCGACAACGGCGTT
GACGTTAACTGTCCAACCAAGATGGCAACACTTTGCTCATGCTCGCAGCATATGCAGGA
CATGCTGATGTCGTGCAGGCGTTGATTGAGCGTGGCGCCGATGTGGATCGCGTGAACAAC
CGCAATCAGACGCCGCTGGCGGGCGCGATCTTTAAGAAGGAAGAAGCCGTCATTGAGGCA
CTGCTTGCTGGTGGTGCTGACCCATACGCTGGAACCTCAACTGCTGTTGATACCGCCAAG
ATGTTTGGCCGCGAGGATCTCGTAGCTCGCTTCGAGTCA

>RXN02391-downstream
TAGGCCGGTGGAGTGGACCGCTT

>RXN02442-upstream

GCCGTGATGTTGTTGAGCGCGATGTGATTGCCGTATGTGCATGTGAGATTCCGGACGCTG
AGTTCTGCCATTCCCTAATGATAACGGTTATCATTTTTCAA

>RXN02442

ATGAAGTTTTTTACTGACGCCCTCATAGTGCCTTTTGACGTTTTATTTCATCTCCCGCGCC
CTGGTCGCCGGATGCCTGGCCGCAATTTTATGCTCACTCATTGGAACGTGGGTTATTTTG
CGCAGGCTAACCTTTTTTCGGCGACGCTATGTGCGACGGCTTGCTCCCCGGAGTAGCCACG
GCATCACTATTGGGCGGAAATCTCATGTTGCGCGCAGCAATCAGCGCATTAATCATGTCA
GCCGGAGTGGTGTGGACCAGCAGAAAATCCAGCCTCTCCCAAGACGTCAGCATTGGCCTG
CAATTTATTACCATGCTTTCCCTCGGCGTGGTTATTGTGTCCCACTCCGATTCCCACGCC
GTAGACCTCACCAGTTTCCTTTTTGGAGACATTCTTGGCGTGCGACCCTCGGATATATTC
ATCATCGCCATTGCAACAGTGTTGGGTGGATTGACTATTTTTCTCTCCACCGACAGTTC
ACTGCACTCGCTTTTCGACGAGCGTAAAGCTCACACCTTAGGACTCAATCCCCGCTTTGCA
CACCTACTCATGCTGGCACTGATCGCATTAGCTACGGTGGTGTGCTTTTCAAGTGGTGGGA
ACGCTTTTAGTGTTTGGACTTCTCATTGGTCCGCCCCCACGGCTGCACTTTTAGTGCAA
GACAAAGCAAGTATTTCACTGATCATGATCGTCGCGTCTGCTTCTTGGATGCGCGGAAAT
TACCTCGGGCTTTTAATCAGCTGGCAGCAGCAAGCACTGCCGCGGGAGCCACTATCACTTTG
TTAAGTGCTGCGATATTTTTTGCCACCTTATTGACAAAGAGTGCCATTAGTAGGTTAAAC
TTCACCGCG

>RXN02442-downstream
TGATACTGAAAGACATTTTCAAT

>RXN02447
ACAGTAGTTCGGGTGTACCTCGCTGAACTCGCACCCTAGAAAATCCGCGGCTCCCTGACC
GGCCGAAACGAGCTTGCTATCGTCACCGGCCAGCTGCTTGCCCTTCGTGATCAACGCGCTT
ATCGCCGTCACCCTACACGGAGTTATTGATGGAATCTGGCGCATCATGTTCCGCGTCTGT
GCCCTCCCTGCCGTCGCCCTCTTCTCGGCATGCTGCGGATGCCGGAATCACCACGCTGG
CTGGTCAACCAGGGGCGTTACGACGACGCCCGCCGCGTCATGGAGACCGTCCGTACCCCT
GAGCGTGCGAAAGCCGAAATGGATGAAATCATCGCGGTGCACTCTGAAAACAATGCGGCA
CTTCCTGGTGTAAAGCAGTCTTCGGGCCAGGCTTCAGGCCAGGTTCTAGCAAGCACACC
CACATGTCCATCGGCGAAGTCCTCAGCAACAAATGGCTGGTTCGTCTGCTCATCGCCGGC
ATCGGTGTTGCAGTTGCCAGCAGCTCACCGGCATCAACGCCATCATGTACTACGGAACC
CGCGTCTCGAGGAATCCGGCATGAGCGCAGAAATGGCTGTGGTTGCCAACATTGCTTTC
GGTGCCGTTGCCGTCATCGGTGGACTGATCGCACTGCGCAACATGGACCGCCTGGATCGC
CGCACACCTTCATCATCGGCCTGTCACTGACCACCACCTTCCACCTTTTGATCGCAGCT
GCCGGCACTCTCCTTCCAGAAGGTAACCTCCATTGACCATTCGCCATCATGATCCTTGTT
GTTGGGTTTCGTGCTCTCCATGCAGACTTTCCTCAACGTTGCAGTGTGGGTGTGGCTGGCG
GAAATCTTCCCAGTCCGAATGAAGGGTATCGGCACCGGTATTTCCGGTATTCGCGGTTGG
GGCATCAATGGCGTCTTAGCGTTGTTCTTCCCAGCACTGGTCTCCGGCGTGGGTATCACC
TTCTCCTTCTTATCTTCGAGTCGTCGGAGTCATTGCCCTGGCGTTCGTACCAAGTTT
GTTCTGAAACCCGTGGCCGCTCACTTGAAGAACTCGATCACGCAGCATTCACCGGCCAG
ATCTTCAAGAAGGCT

>RXN02447-downstream
TAAACCCCTCCGATCTCTTTGG

>RXN02455-upstream
AAGCCTTCGTTATGGGAGGTCTCCAGACACAATCGAATACGGGCCGGATATCCATCTCG
GCTCATCACCCGCTTTTTATCAAGAAAGATGAGGACCTC

>RXN02455
TTGAAGCGTCTTACTCGCATCGCATCCATCAGCATGGCCTCCATGCTCGCCGCCGCAAGT
CTCGTCGCGTGCTCCGGCTCCACCGACGAGGAAGGCGATGTTTACTTCTGAACTTCAAG
CCTGAACAGGACGTGGCATAACAGGAAATCGCAAAGGCCTACACTGAAGAGACCGGCGTT
AAGGTCAAGGTGCTTACTGCCGCCCTCCGGCTCCTATGAGCAGACCCTCAAGGCCGAGATT
GGCAAGGACGAAGCCCCGACTCTCTCCAGGTCAATGGCCCAGCCGGCTTCATCACTTGG
CAGGACTACATGGCAGATATGTCGGACACCGAGGTAGCTAAGCAGCTGACCGACGACATT
CCGCCGCTGACCACCGAGGATGGCGAGGTACGTGGCGTTCCGTTTCGCCGTTCGAGGGCTTC
GGCATCATCTACAACGACGAGATCTTCGACAAGTACATCGCCACGTCCGGCGCAAGATC
AAGTCCACGGATGAGATCACGAGCTACCAGAAGCTCAAGGAAGTCGCCGAGGATATGCAG
GCAAAGAAGGACGAGCTCGGTATCGAAGGCGCCTTCGCCTCCACCTCGCTGACATCCAGT
GAGGACTGGCGTTGGCAGACCCACCTGGCCAACGCTCCGATCTGGCAGGAGTACCAGGAC
AAGGGAGTCGAGGACACCAACGAGATCGAGTTCTCCTACAACAAGGAGTACAAGAACCTT
TTCGATCTCTACCTTGAGAACTCCACCGTAGAAAAGTCTCTTGCGCCGTCTAAGACGGTG
TCTGATTCCATGGCTGAGTTTCGCACAGGGCAAGGCCGCTATGGTTTCAAGAACGTAAGTTC
GCATGGTCCCAGATTTCCGAGACTTCTGGCAACGTGGTCAAGGAAGACAAGATCAAGTTC
CTGCCCATGTACATGGGTCTGCCAGATGAAGAAAAGCACGGCATCAACGTCGGTACCGAG
AACTATTTGGGCGTGAACCTCTGAGGCCTCCGAGGTGACCGAGCAGGCCACCAAGGACTTC
GTGGATTGGCTGTTTACCTCTGAAGCTGGCAAGGAGCACGTGGTGAAGGACCTTGGCTTC
ATCGCACCGTTTCGAAAGCTACACCGCTGAGAACACCCCGAATGACCCCTTTCTGAGCAA
GTCGCGGAAGCTATCGTAACAAGGATCTGACCACCTACCCGTGGAACCTCCAGTACTTC
CCGTCCCAGCAGTTCAAGGATGACTTCGGCCAGGATCTGTGCGAGTACGCCTCCGGAAAG
CTGAAGTGG

>RXN02515-upstream
GTGGCTAAGCAGTTACTTGGCCAAGCTGGGCGGCAGAAAAACCGGCCAGCTAATACT
TCAGTTTAAATTCGCTTCAACCTGAAAGATTGTGACAG

>RXN02515

ATGAGCACTCTTGAAAATCCGTAACCTGCACGCACAGGTCCTGCCGTCCGATGAGTCCGCT
 GAGCCTAAGGAAATCCTCAAGGGCGTCAACCTCACCATCAACTCTGGTGAGATCCACGCC
 ATCATGGGCCCTAACGGTTCGGGCAAGTCCACTCTTGCTTACACCTTGGTGACACCCA
 CGCTACGAGGTAACCGCAGGCGAGGTCCTCCTCGACGGCGAGAACATCCTGGAGATGGAA
 GTTGATGAGCGTGCACGCGCTGGTCTCTTCTCGGCCATGCAGTATCCAACTGAAATCCCT
 GGCCTTTCCGTTGCTAACTTCTGCGTTCCGAGCGACCGCAATCCGCGGCGAGGCTCCT
 AAGCTTCGCGAGTGCGTTAAGGAAGTCCGCACCGCTCAGGAAGCTCTGGCAATTGACCCT
 GAGTTCTCCAACCGCTCAGTCAACGAAGGTTTCTCCGGTGGCGAGAAGAAGCGCCACGAG
 GTTCTGCAGCTTGATCTGCTGAAGCCAAAGTTTCGCGATCATGGATGAGACCGACTCCGGC
 CTTGACGTGGATGCACTGCGCATTTGTTTCCGAGGGCATCAACTCCTACAAGCAGGAGACC
 GAAGGTGGCATCTTGATGATCACCCTACAAGCGCATCCTCAACTACGTTAAGCCTGAC
 TTCATTACGTTTTTCGCGAATGGCCAGATTGTGACCACCGGTGGCGCTGAGCTTGCTGAC
 AAGCTCGAGGCTGACGGCTACGACCAGTTTCATCAAG

>RXN02515-downstream
 TAACATGTCCGATTTCCTCAATG

>RXN02549-upstream
 GCAGTCGCAGTAGTTGGGGTTTCAATGATCTCAGGGCAGGACACTGTTCCCACTGGTAAC
 GCCGTAACCTGCAGACGATGCCCTGCTCGGTGGCCCTGAGT

>RXN02549
 ATGGTTCACGCGAAGCAGACTAAGAAGCCACTTCCCCGTTTTCTTCACTCGGCGCATTTT
 TATGTCTGGATTGTGCTGGGTTTTGTGGTGTTCGCAACCTTATGGTCAGGTTGCTGCC
 GATACTAACTAGATTTGCTGCTCAACCCCGCAGGATTTTTAACCAGGTGCGCTTCATGCG
 TGGACTGACACGTTACCTTGGGTGAGTTGCAAAACCAAGCTTATGGCTATCTGTTTCCC
 CAAGGGTTTTTCTTCTCATAACTGATTTCTCCCTGACTGGATTGCGCAGCGACTGTGG
 TGGTGGCTTGTCTTGGCCTGGGATTTTCTGGATTCTACGCACTGGTAGCCCGGTGGGG
 ATTGGCAATCCTGCATTCAGGGTGATCGCCGCGCTGCTGTTTGTCTGTCCCCGCGCACG
 CTCACCACTCACTGCAATCTCTCCGAAACTTGGCCTATCATGCTCGCGCCATGGGTA
 TGTCTGCCCTGTGTTTTCGGAAATGTGGATGCACGGGCCATCGCGTTGTCTTACTTCCC
 GCGGCATGCATGGGTGCAGTTAATGCCACCGCCACGATGGCAGCACTCATCCCCGCGAGCG
 CTGATCTTGCTGTATAGAGGGCTCTTCTTAAGGCTGCTTCTGTGGGAATGGGCGTTCTC
 GCTGTTAATTCATGGTGGATCGGACCTTTGTTGGTGTCTGGCAAATACGCCCCGCCCTTC
 ACCGAATTCATCGAAAGTTTCTCCGTACCACTTCTGGCTCAACCCAGTAGAAATACTC
 CGCGGAACCAAGTTGGACACCTTCTGATGACACTGAACGACAAGCCGGATATCTCCTG
 GTCAACGATGCTCTCTTTGTCACCTCAGCGTTCTCGTCGACGCCCTCGGCTTGATCGGC
 CTCACCTTGATGAAACACCGTGGACTGTGGGCATTTCATGCTGGCCATCGGACTCCTCATC
 CTCGGCAGCGCCCACTAACGGCTGTTCAAGAATTCTCGACGGCCAGGCGCAGCACTT
 CGAAACATCCACAAATTTGATCTATTAGTCCGCATGCCGTTGATGGTGGGCGTTGCCGCA
 TTGGGGTGCATATCAGTCTGCCCTTGCTTGGGACGACTGCATTGACCAGCGGACAAGGC
 AAACACCACACCATCCCGCTGCCCTCTCCAAAACGCCAAGCCGCGAGGACTCCTCGTGGTG
 ATCATCGCTGTGCGTGTCTTGCTCCCGCATGGTGGCACGGCTGCTACCTCAGGGAACG
 TGGGATGAAGTGCTGACTACTGGTACGAAGCCACAGAATTCCTCAACCAAAACGCCACA
 GGCACCCGACGTTGATTTGGCCTAGCTCGCCGTTTGGCCGCCAGGACTGGGGATGGACT
 CGGGATGAACCAGCTCAACCACTTCTTGATGTTCCGTGGGCTGTCCGCGATGCCATTCCT
 TTGGTTCCCCCGGAGGCGATTTCGCGGATTAGATGGTCTCGACGACCTAGGCACTCTAGGC
 ACCGGTCTAAACGACGAGGCTTTAAACGCTTAGGCATCGGCGCAGTACTGGTGAGGCAT
 GATCTGGAAGCCGACCCAGATATTGAGGTGGATCTGCCTGGGGAAAAGCACACTTTTGGC
 TCCCAAGGCCAAGTAGACGTCTACCTACCGACCCGACCGCAATATGTGGATCACTTCC
 GGCACATCCAAGCAGCTGCCACCGTCTGCTGGCGGCGGCAAAATCCTCTCGCTCCTAGAC
 ACCATCAACGGCTATTCCCCGAGGACTTTGGTGAGTGAGAATGCCAGATCGTCACCGAT
 ACCCCTCAGTAGTCGGCACAAATTACGGCGATGGCACAGTTCCGCGAGCATTTGCCAGC
 CTTGATGAGACTGAGGTGAAAAACCGCATCGTGGATTATCCTTCCGCGGGGCCAATGACG
 CAGGTGGTGCAGGAAGGTTCCATCACGGCGTCTTCGTCTGGTTCCGATGCCACTTCTTTC
 GGC GGCGCGGATCCTGATCGTTCCCTTAATTCACTTCTTGATCATCGTTACAACACCGCC
 TGGTACCCGACACCTGGCGATACGTCTCCGTGGCTCGAAGTCTCCGGTACCGGCACCACA
 TTATCGATCTCCCCCGCAGCACCGTCAACCGCCACCATCACCTCCGGCGATTCCGTGATG
 GTCCGCGAGTTGAAAAAGGCCGACCAACACAGTTACGTTGGCGGAGCCTGAAGCTCGC
 ATTGAATTCGATGGTTTTCGTAGGAATTTCCGAGCTGTCCCTAGAGGGTCTCAGCCGCACC
 ATCACTGTGCCGAGACCTCTCCTGACGTGCAGCAATTTCGTTTTCCAACGCCTCACAGTG

CCCACCTCGTTCTCGACCGCACTTTACAGTCCCCGCCACATGTCCGTACCGTGGAG
 GCCCAATCCTGCGTCACATTGGAACTCGACGGCGATCGCATCGACTGTGGCCCCCTCGAAC
 TCACCCCCGGAACCCACACGCTGCGCACCCAATCGGAATGGGTACCCCTACCCGAATCCG
 CTCCGCTCGCCGCTGTTAGCCAGCAACAAACATCGAGGCGACCCACCGACCGCGTGC
 TCGTACCACGCGCGCTTTCAATTACAGGTACCAGCGCGCTTATCGACGCCACCCCCCTTT
 CCCCAAATCCAACTCGACGCCTCCTCCCAAGGTTTCATCATCCCCGCGAACGCCTCCGGCG
 AGT

>RXN02549--downstream
 TGAGCTTCGCTTTCGACGGCGAA

>RXN02570--upstream
 CCATTGTTATGCTCATTGTGTTTGTGGTGGTCAAGTCGCTACCCAAGCGCACCACTAGGG
 CATTGGTTCGCGAGCGGGTTCGGGAGGACGTGCTTAAAC

>RXN02570
 ATGAATCCTTTGACATGGATCATTGGCGCATTACAGCATGTGGATCGTGGTGTGGGCGTT
 AATAAGCTTGGTTTAAAGCATCGCAGTGATCATCATCGCGCAGGTCGTGGCGATGATTCCG
 GTGCGCAATGTATCTGTGTTGGCTTCAACAGCATTGTTATCGGTTCTTGCATTGGCCTCG
 ATGGCGCTGATTCACATGCCGATTCTTCCGACGGCTGGTTGATTGCTCTTACCTTGACG
 GCTCGTTTTAGTGCGTTGATGTCTATTTTCTCCTTGCAGCAACAGCGATTACTATTCCT
 GAGCTGGTGAAATCCCTATATCGTTGGCCCAAGCTGGCGTATATCGTGGGTTCTGCATTG
 CAGATGATTCCGAGGGTAAACAGACCTTGGCGTTGGTTGTTGTTGTTGTTGTTGTTGTTG
 GGGCGCAGCGTTAAAGGTCCCGTGCGCGCGGTGAAATATGTGGGTTTGCCCCGTGATTACA
 CATTTACTTAGTGCAGGTGCCGCGCAGCGATTCCCTTGGAGGTGCGAGGCCTGGACAGG
 CCGGGGCCGCGTACGGTGTGTTGTTGAGGTGGTGGAGGGGCGCGTCGAAAAGCATTGTGCG
 TGGTTGTTGCCGCTTTTGGCAGTCGGGATGGCGTGGTGGCTC

>RXN02570--downstream
 TAACTCAAATCGTCGGACCGTCC

>RXN02595--upstream
 GTGGGTAAAGGGGACTCCGAGGAAGTCCACGTGCTCTTCTTTTCGCGGCGCTGAGGATGGT
 TTCGCGGATTGTGCGGGGGAGTGGGTGGGAGAGAAAACG

>RXN02595
 GTGATCGTTGTGGCCATGGCTTCCATTATGGCTTGTTTAAAAGCAGCTAGACTGAATAAC
 CCTATGAAGATCCTTTTGTGTGCTGGCGTGATACCACTCATCCTCAAGGTGGCGGAAGT
 GAACGCTATCTGGAGCGGGTGGGTGAGTTTTTGGCGGATCAGGGCCATGAGGTGGTGTTT
 CGTACTGCTGGGCACACGGATGCGCCACGGCGTTCTTTCCGCGATGGTGTGAGGTATTCC
 AGGAGCGGTGGGAAGTTTAGTGTGTATCCCAAGGCGTGGGTGGCCATGATGTTGGGTGCT
 GTGGGGATTGGCACGTTTTTCCAAGGTTGATGTGGTGGTGGATACGCAGAATGGCATTCCG
 TTTTTTGGAAAGTTTTTCTCCGGTAAGCCGACTGTGTTGCTCACGCATCATTGCCATAAG
 GAGCAGTGGCCGGTGGTGGGTGCGGTGCTGGCGAAGGTTGGTTGGCTGATTGAGAGCCAG
 ATCGCGCCGCGCGCTTACAAAACGCGCCGATGTGACTGTTTCAGAGCCGAGCGCTGAG
 GAGCTCATTGCGTTGGGTGTGGATCAGCAGCGGATTTCATATCGTGCACAATGGCGTGGAT
 CCCGTGCGCGCTGCACACGCCGAAGCTGGATCGCGATGGCCAGCATGCGGTGACGTTGTGCG
 CGCCTGGTTCCGCACAAGCAGATTGAGCATGCGATGGATGTGCTGCGGGCGCTCGACGGC
 GTGGTGCTGGATGTAGTCGAAAGCGGTTGGTGGCAGAAGGAAGTGGTCGATTATGCCCGC
 ACGCTGGGTGTGAGCGATCGCGTGGTTTTCCACGGCCAGGTCGCCGAGGATCACAAGCAC
 GCCCTGTTGGAGCGCGCCACGATTTCATCTCATGCCTTCGCGCAAGGAAGGCTGGGGCCTG
 GCGGTACGGAGGCGGCGCAGCACGGCGTTCCGACGATCGGTTACCGAAGCTCAGGCGGC
 CTGCGCGATTCCGTCGTCGACGGCGAAACCGGCCTGCTTGTGACTCCAAGGCCGAGCTT
 ATTTTCAGCCACCAAAACCCTGCTTATCGACGCCTCCCTCCGCTCCAAGCTCGGCGCCAGC
 GCGAAGCAGCGCGCCGAAAACTACAAGTGGGACACCGCGGGAGCGCAGTTCGAGGAACCTA
 CTTCTTGGTCTTGGCTCGAAAAAG

>RXN02595--downstream
 TAGTCCCAGCGGCAACGCCATCC

>RXN02614--upstream

TCATTGTATACGCCACCCTCGGTCTGCTGTCTGAAGCGCTGATCAGAGCTTGGAACGTC
ACACCTTCCGCTACCGAAACGCATAAGAAAGTTGCTCGCC

>RXN02614

ATGACTGCCACATTGTCACTCAAACCCGCAGCCACTGTCCGTGGATTGCGCAAATCATAC
GGAATAAAGAAGTCCTCCAAGGAATCGACCTCACCATCAACTGCGGCGAAGTAACCGCG
CTGATCGGACGCTCAGGTTCAAGAAAATCCACCATCCTGCGCGTGTGGCGGGCCTATCT
AAAGAGCATTCGGGCTCTGTAGAAATTTCCGGAACCCGCGCTTGCCTTCCAAGAGCCT
CGCCTGTTGCCGTGGAAAACGGTGTCTGATAATGTGACCTTTGGCCTCAACCGCACTGAT
ATTTCTTGGTFCAGAAGCACAAGAACGCGCCTCGGCACTGCTTGCAAGAAGTCAAACCTCCC
GACTCCGACGCCGCTGGCCCCCTCACGCTCTCCGGCGGCCAAGCCAGCGCGTCTCCCTT
GCGCGAGCGCTCATCTCCGAGCCAGAGCTTTTGCTTCTCGACGAACCCTTCGGCGCCCTC
GATGCTCTGACAAGACTGACAGCCCAAGACCTGTGCTCAAAACCGTGAACACCCGAAAC
TTGGGAGTTCTGCTGGTCACCCATGATGTTTCCGAGGCCATCGCCCTGGCCGACCACGTC
CTTCTTCTTGACGACGGCGCCATCACACACAGTTTGAAGTGTAGATATCCCCGGCGATCGC
CGCACCCACCCCTCCTTTGCCTCCTACACCGCTCAACTCCTTGAGTGGCTCGAAATCACC
ACACCTGCC

>RXN02614-downstream

TAGAAAGAAATCATGAAATTTAA

>RXN02795-upstream

GCGGTGTGGCCCGGTGCTGCGATCGCTTTGACGGTCCTTGGTTTTAATCTTTTCGGTGAT
GGTTTACGCGATGCCATCGATCCAAAGCGGGAGGTGCGCC

>RXN02795

GTGCTTAAAGTTTCTGATTTAACGGTTGGCAACAATTTTGTCCACAACGTCTCCTTCGAG
GTCAACCCCGGCGAACGCGTCGGCATCATCGGCGAGTCCGGCTCAGGCAAATCACTCACC
GCGCTATCCATCATGGGTTTAACTGACCTGCCGACCACCGGCCAGATCACCTTCAACGGC
AAACCTCCCGCTACATTCCGTGGCACCAGCATCGCCATGGTTTCCAAGAACCAATGAGC
GCACTCAACCCGCTCATGCGCATCGGCGCCAAATCGAAGAAATGATGACCTGCACGGG
GCAAGCAAAAAAGACGCGCGGGCGCGCTTAAAAAGCTTGCTTATCGACGCTCTCCCTCCCC
GAACGCACCGCTTCGGCCTACCCACACGAACCTTTCAGGCGGGCAACGCCAACGCGCACTA
ATCGCAATGGCGCTGGCCAATGATCCTGACCTGTTGATCTGCGATGAACCCACCACGGCT
TTGGATGTGGTTGTGCAAAAACAAATCGTCGATCTGCTGCTGCGTCTCACCAAAGAACGT
GGCACCGCTTTATTGTTTCATCACCACGATCTTGGACTCATCGCGCGCACCTGCGAACGC
TTATTGGTGATGAAATCCGGCGAAACCGTAGAACGCGCGACACCGAGGCAATTCCTTCGC
TCCCCCGCCCATTCGTATACCCAACAGCTCCTTGATGCTTCAATCCTTGACCAGCCAGAA
ATCGCCTCAGATTCTGGCGCGCCGTTAGTGATTGATGTGGAGGAGGCGTCGAAAAGCTTT
AAAGAAACCACCGCCCTCCACAAGGTTTCATTGGCGGTGCGCAAAGGTGACCTGCTTGA
ATAGTCGGCGGATCAGGTTCCGGGCAAAACGACTCTGCTGAAGCTCATCGCCGGTTTGGAT
AAGCCCACAACCGGTACCGTTGCGGTAACCGGTGGTGTGCAGATGGTGTTCAGGATCCC
CAATCAAGCCTCAACCCACGGATGAAAATCAAAGACATTGTGCGCGAACCCTGCTTGGT
TGGAACGCGGCGGAGAAAACACACGGGTTGCGGAAGTCATACCCAAGTGGGACTGAGC
CCCGATGTCTTAGATCGCTACCCCCACGAATTCCTCGGAGGACAGCGCCAACGAATCTCC
ATCGCCAGAGCCCTCGCCATCAAACCAGCGATCCTGCTTGCCGACGAACCTGTCTCCGCC
CTCGATGTGTCCGTACGTAAACAAGTACTGGATCTTCTCCAACAACCTCGTCGAAGAATAC
GGCATCACCTTGGTGTTCGTCTCCACGATCTGGCAGTGGTGAGACACCTGTGCACAACC
GTGTGGGTGATGGAACAGGGACGAGTCCTTGAGCAAGGGCCCATCGATTTCGGTTTATGAT
CACCCACAGACCGAATACACCAAGGAGCTGCTTGATGCCGTTCCGCGGTTGAGCCTT

>RXN02795-downstream

TAAACCAGCGCAGATGACAACGC

>RXN02925-upstream

AAACCGTCCACCGGGCAATTGAGGAGACCGGCTACACCGTCTTGCTCTGATCGATTACCC
CATCATCTCGACCCCGACCGGTTGAGCGGAAGGAACCTC

>RXN02925

ATGAGCACTCCCCACCACCACGGTGATCACCCCGCTCCGGAACAGACCACACCCACCAC
CCGAATCATGCCGGTCACGAGCACCATGCGGATGCCGCCACCCACGGCCAGGCCATGCCG

CACGATCATCCGCATTCCACTGTCGATGAAGAACATCAGGTCCACAGTCACGGTGAACAC
GCCGGCCACAGCGCCGCGATGTTCCGGGACCGCTTCTGGTGGTCGCTGATCCTGTGGTT
CCGGTGGTGTCTTTCAGCCCGATGTTCCGCGACCTGCTGGGATATAATATTCCGGAGATT
CCGGGAGCCTACTGGATTCTTCCGGTCCTGGGCACGATCATCTTCTCTACGGCGGCACC
CCCTTCCTCAAGGGCGCAATGACCGAGCTGAAATCCCGCCAACCGGGCATGATGCTCCTG
ATCGCCATGGCGATCACCGTGGCGTTTATCGCCTCCTGGGTCAACACCCTGGGGCTGGGC
GGGTTCACCTAGATTCTGGTGGGAACTGGCCCTGCTGGTGACCATCATGCTGTTGGGC
CACTGGCTGGAGATGCGCGCTCTTGGTGCAGCCTCCTCCGCGCTTGACGCGCTGGCAGCG
CTCCTGCCGATGAGGCCGAGAAGGTGCTCGACGGGACCACCCGCACCGTAGCGATCTCA
GAGCTGGCCGTCGACGATGTCGTGCTGGTCCGAGCAGGTGCCGCGTCCCGGCCGACGGG
ACCATCATCGACGGAGCGGCCGAATTGATGAGGCCATGATCACCGGCGAATCCCGACCC
GTCTACCGGGATACCGGTGAGACCGTGGTGGCCGGCACCGTGGCCACCGACAACACCGTC
CGTATCCGGGTGGAGGCCACCGGTGGGGACACCGCCCTGGCAGGCATCCAGCGCATGGTC
GCCGACGCCCAGGCCCTCCTCCTCCCGGGCCAGGCCCTGGCCGATCGAGCCGACGCTTA
CTGTTCTGGTTCGCCCCTGATCACGGCCCTGATCACCGCCGTGGTCTGGACCATCATCGGC
AGCCCCGACGATGCCGTGGTCCGCGCGGTGACCGTGTGATCATCGCCTGCCCGCACGCC
CTGGGCTGGCCATCCCGCTGGTCATCGCGATCTCCTCCGAGCGCGCCGCGAAATCCGGG
GTGCTCATCAAGGACCGCATGGCACTCGAGCACATGCGCACCATCGACGTCGTCTTGTTTC
GATAAGACCGGCACCTGACCGAAGGCGCACACGCCGTACCGGCGTGGCTCCGGCCACG
GGTATCGCCGAGGGTGAGCTGCTGGCCCTGGCCGCCGCCGCTGAGGCCGATAGTGAGCAC
CCCGTGGCCCGCGCGATCGTGAATGCCGCGGCCGACACCCGGAGGCCCTCGCAGCGTCAG
CTGCGCGCAACCGGTTTACCGCCGCTCCTCCGGCCGCGGGATCCGGGCCACCGTCGACGGT
GCCGAAATCCTCTGGGCGGGCCGCAACATGCTACGCGAGTTCAATCTGACCACCCCGGGT
GAGCTCGCCGACATCACCGGTTCTGGGCACAGCGAGGTGCCGAGTGCTACATGTCGTC
CGCGACGGTGAGATCATCGGTGCGGTGGCAGTGAGGACAAAATCCGCCCGAATCCCGC
GCGGCGGTACGCGCCCTGCAGGCCCGCGGGGTGAAGGTGGCGATGATCACCGGTGACGCC
ACCCAGGTGCGCCAGGCAGTGGGCAAGGATCTGGGGATCGATGAGGTCTTCGCCGAGGTT
CTGCCGAGGACAAGGACACCAAGGTACCCAGCTGCAGGAGCGCGGTCTGAGCGTGGCC
ATGGTGGCGACGGTGTCATGACGCCCGGCCCTGGCCCGGGCCGAGGTCCGGTATTGCG
ATTGGCGCGGGTACAGATGTGGCGATGGAGTCCGCCGGGGTGGTCTGGCCAGTGATGAT
CCCCGGGCCGTGCTGTGATGATCGAGCTCTCCATGCCAGCTACCGCAAGATGGTCCAG
AACCTGGTCTGGGCGACCGGGTACAACATCGTGGCCGTTCCGCTGGCCGCGGTGTGCTC
GCCCCATCGGTGTGCTGCTTCCCCCGCGCGGCCGCCATCTTGATGTCCCTGTCCACG
ATCATCGTCGCCCTCAACGCCCAGCTGCTACGCCGATCGACCTGGACCCGGCTCACCTA
GCTCCGACCGACGGGAAGGAGGAGAAGGCTGCTGTGAGCTCTGCAGCCCCCGTCCGC

>RXN02925-downstream
TGACTTTCAATGCTTCATGGACT

>RXN02933-upstream
TGATCTGCTGTATCAGGTGGTTGATCCAAGAGTCGGTGCTGTTGGGGTTGCTAGCACTAA
GGTTCAGGGAGCGTGGCTTAAGTGACAACGATCAAAAAC

>RXN02933
ATGCCCCCTTTAGGGAAAAATCGGCGGCTTCATCGTTGCCGTTGTATTTGTTCTTGCTGCG
CTGTCTTTTCATTTGGAATCCGTTTGATCCAGTTCAAGCTTTCCACAGGAGCGCCTTGAG
GGAAGTTCTTTGAGGCACCTGTTGGGAACGGATCGTTATGGTCCGATGTTTTATCCAG
ATCATGGTTGGTTCCCGCGTCACGTTGTTGGTGGGCATCATTGCGGTGGCGATCGCAGCA
TTAATCGGCACGCCACTGGGTATTGCTGCGGGAATGCGCCGTGGCATGGTGAAACCTTT
GTCATGCGTGGTGCCGATTTAATGTTGGCGTTCCAGCACTGTTGTTGGCGATTATTTCC
GGCGCCGTTTTTCGGCGCCTCCACGTGGTCCGCGATGGTCCGATCGGCATCGCAGGCATC
CCTAGTTTTGCCCGCGTGGCTCGTGCAGGCACATTGCAGGTGACCAGTCAGGATTTTCATC
GCAGCTGCTCGGCTATCAAAAGTAAGTTCCGCCCGGATCGCGCTTCGCCATATTTGCC
AACATCACCAGCATGTTGATCGTTCAGGCATCAGTAGCTTTTGCCCTGGCGATCCTGGCG
GAAGCCGCATTGAGTTTCTCGGTTTGGGCACCACTCCCCCGGATCCAGCTGGGGTCGC
ATGTTGCAAACCGCTCAAGCATCCATCGGCGTCACCCCATGTTGGCGGTGTGGCCCGGT
GCTGCGATCGTTTTGACGGTCTTGGTTTTAATCTTTTCGGTGATGGTTTACGCGATGCC
ATCGATCCAAAGCGGGAGGTCCGCCGTGCT

>RXN02933-downstream
TAAAGTTTCTGATTTAACGGTTG

>RXN02945-upstream
TTCCGGTGCATCCTTGCCGGCCTGCTCAGCTGGTACCTGGTCCGCGCGTTGGCGAGGAC
TGGTGCACTTGATCGTTTCGCCGCTGGCCGCGAGGTATAA

>RXN02945
ATGACCACCGCACTTGGAACGCGCGTTGTTGCGCGCAACTTTGGCTACCGCCATGCTTCC
CGGGAAAACCCCGCGCTCAAAGACATCAACTTCGAGATCGCACCTGGTGAACGCATCCTG
CTCACC GGCGCTTCCGGCGCCGAAAATCCACGCTACTCGCCGCGCTCGCTGGCGTTTTA
GGCGGTTCTGATGAGGGCGTTTCTACGGGCGAATTGCTTGTGACGCCCCCTCCATCGGT
TTGGTTCTCCAAGATCCAGATTCCCAAGTCATCGCCTCCCGCATCGGCGATGATGTGGCG
TTTGGCTGCGAAAACCTCCAAATTCCGCGCGAGGAAATCTGGCCACGGGTGGAACGAGCA
CTTGAATTGGTGGGCTTGGATCTACCACTGAGCCACCCACGAAATATCTTTCCGGTGGC
CAAAAACAACGCCCTCGCTCTTGGCGGTGTGATCGCCATGGGTGCTCGTCTGATTCTGCTT
GATGAACCCACCGCAAACCTTGATCCTCAAGGCCAAAAAATGTGGTCGCAGCAGTGGAT
CGCGTTGTTTCAAGAACTGGAGCAACACTCATCGTGGTGGAAACACCGCCATGAGCTGTGG
GTCAACATCATTGACCGGATCATCAGTATTACTGACGGCGAAGATGTCCAACCTGCAGAG
TTGATCAAGGTGGGCCAGTTGCCCTGGGGCGCAGCCGTCGACAAGCAAACCGATCTTGTGG
GCGAATGATTTGCTGTGCACCTGGGGCGGCCTGCGTAGTTTTGAGGTGCCGGAAGGCGCC
TCGACGGTGATCACCGGGCCGAATGGCGCTGGAAAATCCACACTTGCGCTGACCATGGGT
GGATTGCTTCCGCGAAAAGTGGGCAGCTGGAACCTCTCTGACACGGTGCGCGGCGGCCTTA
ACACGCCCCCGCACAAAGTGGCGTTACAGCTGATC

>RXN02945-downstream
TAGCTGCACGTATTGGCACTGTC

>RXN02975-upstream
TCGTGCGGTGCAGTCCTCGGATTGCTTAAGTTGTAGGTGGCTGGGGGCGTCGAAAAGCAGC
TTTATTGACCTGGCAACTTCAATTGATAGACTGTTAGGTT

>RXN02975
GTGATTGTACCAATGATTTAGAGGTGCGCGTTGGCGCACGTACCCTTCTCGATGCCCCA
GGTCAGCTCCTTCGGGTGCAGCCAGGCGACCGTATTGGTCTGGTTGGTAGAAATGGTGC
GGCAAACCAACCATGCGAATCCTCTCGGGCGAAACCAAGCCCTACGGAGGATCCGTA
ACCACATCTGGTGAAATCGGTTACCTGCCCCAGGACTCCCGCGAAGGCAACATCGAACAA
ACCGCCCGC

>RXN02994
ATCAAGATGACGGGAGTGCAAAAATACTTCGGCGACTTTTCATGCCCTTACGGATATTGAT
CTTGAAATTCCCAGAGGACAAGTTGTCGTGCTACTTGGACCATCCGGATCCGGCAAGTCA
ACCCTTTGCCGCACGATCAACCGTCTCGAAACCATCGAGGAAGGCACCATCGAAATCGAT
GGAAAGGTTCTCCCAGAAGAAGGTAAAGGCTTAGCCAATCTCCGCGCCGATGTCGGAATG
GTATTCCAGTCTTTCAACCTCTTCCCCACCTCACCATCAAAGACAACGTCCTCTTGCA
CCCATCAAAGTGCGAAAGATGAAAAAGTCTGAAGCCGAAAGCTTGCGATGAGCCTGTTG
GAACGCGTCGGCATCGCAAACCAAGCTGATAAATATCCGGCGCAACTGTCCGGCGGTGAG
CAACAGCGTGTGGCCATCGCGCGCGCACTTGCGATGAACCCAAAGATCATGCTTTTCGAC
GAGCCCACCTCCGCCCTTGACCTGAAATGGTCAACGAAGTGTGGACGTCATGGCAAGC
CTTGCCAAGGAAGGCATGACGATGGTGTGTGTTACCCACGAGATGGGATTGCGACGCAAA
GCAGCCGATCGTGTGTTGTTTATGGCGGATGGGCTCATTGTGGAAGATACGGAACAGAT
TCCTTCTTACCAACCCTAAGTCTGATCGTGCAAAAGACTTCCTCGGCAAGATCCTTGCC
CAC

>RXN02994-downstream
TAGTTTTTGGCTGCGCCTCTATC

>RXN03020-upstream
CGCCGACGAGGACTCATCGGTGCCGCCATTTCACTCGGCCCATCCTTCGCGTCAACC
ACGCTCCGCACTCATGAACGCATAAGAAAAGGAACCTCAC

>RXN03020
ATGACTCTCCAGTTTTCAAATCTCAATCTGACCGTCGCCGACGGATCCACCTCACGCACC

CTGCTCAACAACATACACTTTTGGATGTCCAACCAGGCGAAGTCGTGCGGTATCACCGGCC
 CATCCGGCTCCGGAAAATCCACCCTACTCGCCGTCTCTCGGCTGCCTCCAAAGCGCCCGAT
 TCCGGCACCAGCGACGCTCGGCGACATCGACCTGCTCAACCCCCAAAACCGAGCTGCTTTA
 CGACGCAACCACCTAGGAATTGTCTTCCAACAGCCAAACCTGCTCCCCTCGTTGACTGTC
 CTCGACCAACTGCTGCTCATTCCCCGGCTCGGCAGGATCCTCCCGCCCAGCCGCGAGCGCA
 CGCACCCAAACACAAAGACAAAGCCCTTTCACTTCTGAACTCCATCGGACTCGGCGACTTA
 GCAAAACGCAAGGTCAGCGAACTATCCGGTGGACAACAAGCCCCGCGTTAACTTGGCCCCGC
 GCGCTGATGAACTCCCCAAGCTCCTGCTTGTGATGAACCCACCGCCGCCCTCGATCAA
 CATTCCGCCAGCGAAGTCACCGAACTAATCGTCTCGATGGCCCACCAATACAACGCCCC
 ACA

>RXN03080-upstream

CTTGCAAACAGGCGTGGTGGCTTCATTGGCTCACCAATTTTCCTTTATTACTGCT
 CAGCATGCGCAAGCGACGCGGATTGGGGCTGTAAAACTC

>RXN03080

ATGCCTCAATTAGTTGAAATTCGTGATCTCAACGTTGAATTCCCCTCTCGCCATGCAGTG
 AAAAACGTGTCTTTTCTGCACCTGCTGGAAAAGTCACCGCACTGATTGGCCCAAATGGT
 GCTGGTAAAAAGTACTGCCCTTTCGGCGATTGCAGGATTGGTTGAATCCACCGCGCAGGTA
 ATGGTTGGTGGGAGTGGGGTTGCGTCGAAAAGCGCTAAAGCCCCGAGCCCGCCTGCTCTCA
 CTCGTGCCGCAAAAACCCGAGTTGCGCATTGGTTTTAGTGACGCGACGTTGTGCGGATG
 GGCCGCTACCCCGCATCGTGGCCGCTTCGCCGTGGAGACCGCAGATCGACGCGCCACC
 GATGACGCCCTGCGCGCCATCAACGCGCTCGACATCGCCGAGCAGCCCGTCAACGAATTA
 TCGGGCGGCCAGCAGCAGCTCATCCACATCGGCCGAGCGCTCGCCCAAGACACCGCCGTC
 GTGCTTCTCGACGAGCCCGTCTCCGCCCTTGATCTACGGACCAAGTTGAAGTCCTTCAA
 CTCCTGCGCGCCGAGCTAATTCCGGCACCACCGTGATCGTCTCCTCACGATCTCAAC
 CACGTTGCCCCGTTGGTGCAGCATGCAAGTTGATGGCCGACGGCGAAGTTGTCTCCCAA
 GGTGACATCCGCGAGGTGCTCGAACCTGCCACACTGTCCACCGTGACGGACTGCCCAT
 GCGGTGCGCGATGATCCCGAAACCAGCTCACTTCGCGTGATCCCGCATCCAAATCCCTTT

>RXN03080-downstream

TGATTGAAAGTTTGACTTAAAAA

>RXN03081-upstream

ACGGACTGCCCATTTGCGGTGCGCGATGATCCCGAAACCAGCTCACTTCGCGTGATCCCGC
 ATCCAAATCCCTTTTGATTGAAAGTTTGACTTAAAAACCC

>RXN03081

ATGAAAAAATCACTCATCGCCATTGTTGCCAGTGCGCTCGTGTTAAGCGGCTGCACCTCT
 GATTCTTCTGACTCTTCCGGCACTTCCGGAAGTGTGGAAACCACTTCGATTACAAACCAGC
 GTTGCCGCGAGCTGACGGCGCATTTCCACGCACCGTCACACTCGACGATTCTCCATCACC
 TTAGAATCCAAACCAGAGCGCATCGCCGTACTACCCCAGAGGCAGCATCCTTGGTTCTC
 CCCATCACAGGCGCCGACCGCGTCGTGATGACCGCCGAAATGGACACCGCTGACGAAGAA
 ACCGCAGCTCTGGCCTCCCAAGTGGAATACCAAGTCAAAAACGGTGGCAGGCTCGACCCC
 GAACAAGTTGTGCGCGGCGACCCAGATTTGGTGATCGTCAGTGCGCGTTTCGATACCGAA
 CAAGGCACCATCGACATTTTGGAAGGCCTCAACGTCCCG

>RXN03081-downstream

TAGTTAACTTCGATTACAGACGCT

>RXN03108-upstream

CAACCAGCCTGCCACGTTGCTGGATGGACCGTCGTAATCATCGGCATCACCGGCTTAATC
 CTTGACCACCTCATCGGTGAGTTGCAGAAAGTAGTTCGCT

>RXN03108

ATGACTAAACCAAACGCTTCCGTGAGCTGAATACGATCACCAAGTCCTACGGCTCCACC
 ACTATCATTGGCGATACGAGCATCACCATCAACGACGGTGAATTTCGTCTCCCTCCTCGAC
 CTTCCGGCTGCGGAAAATCAACAAATCTCAAAATGATCGCCGGAAGTGGCCTCCCCATCC
 ACCGGCACAGTCAGCGCAGGCAACGAAGAAATTAAAGGACCAGGACCTGACCGAGGCATG
 GTTTTCCAAGACCACGCCCTCCTGCC

>RXN03108-downstream
TGATTGACCGCACGCGGCAACAT

>RXN03116-upstream
AGGGGAATGGCTTAATATCGTAGGTCCCAACGGCTGCGGAAAGAGTACGTTGCTGCACGC
TTTTGCTCAGGTACTGTCACTGGAATCGGGAAGGCTGAAA

>RXN03116
ATGGGGGAGGGGGACGTCGAAAAGCATTGCTTTTGGTCTTAAAGCTGCGAAGCAGCGT
CGCTTTTCGCGCGTACCGTGGCCCTCATGCCACAGAATCCTACTATTCTGCAGGTCTG
AGCGTTTTGATTATGTGCTGCTGGGGCGTCATCCGCACAGTTACGCGCCGGGGCGTGCT
GATGATGAGATCGTGAAGCGGTGCCTCGCTGATCTGAAATTGGAGCATTTCAGCGACCGC
GGCTTAGACGAATTGTCCGGCGGCGAGCGTCAACGCGTCAGCCTTGCCCGCGCGCTCGCC
CAAGAACC CGCATCGTGCTTCTCGACGAGCCGACCTCCGCGCTTGACATCGGCCATGCG
CAGGAAACGCTTGAGCTTATCGACGCCATCCGGCACCGACTCGGCCTCACCCTGATCGCG
GCGATGCATGACCTCACCCTGACTGCGCAATACGGCGATCGGGTGCTCATGATGAATGGT
GGCCGCAAAGTTTTCGAGGGCACTGCAGCCGAAGTGCTCACC CGCAGCGGATTTCCGAG
ATTTATGATGCCACTGTGATTGTTGAGGTTATTGATGGGCGTCCCGTGGTGATTCCGCAA
CGGTGCGCAC

>RXN03116-downstream
TGACCTGTTGTGGCAGACCAGAC

>RXN03129-upstream
GCTGAGGTTGAGACCAAGCTGAACACCATCTACACCCGCGACATCGAACCCTTATTTAA
TCCGAGCACTTCAGCTACACCTATTTAAGGAGGCTGTGAC

>RXN03129
ATGGCGTCAATCGTCTTTGAAAACGTCACACGCAAATACTCTCCGGGCGCACGCCCCGGCC
TTCGACAAGCTTAATTTGGAAATCGCCGACGGCGAGTTCCTAGTTCTCGTTGACCCTCA
GGCTGTGGAAAGTCCACTTCTTTGCGCATGCTGGCTGGTCTTGAGCCTATCGACGAGGGA
CGTCTACTCATTGATGGTAAAGACGCCACGGAAGTGCCTCCGAGGATCGTGACATCGCT
ATGGTCTTCCAGAGCTACGCGCTGTACCCGAATATGACTGTTCCGGGACAACATGGGCTTT
GCGCTGAAGAATCAGAAGGTGGCTAAGGCTGAGATCGAAAAGCGTGTTGCTGAAGCCTCA
CGCATTCTGCAGCTGGATCCGTATCTTGATCGTAAGCCTGCAGCTTTGTCTGGTGGTCAG
CGCCAGCGCGTGGCCATGGGGCGTGCAATTGTGCGTGAGCCATCGGTGTTCTGCATGGAT
GAGCCACTGTCCAACCTAGATGCCAAGCTGCGTGTGTCTACGCGTGCGGAGATCTCTGGT
TTGCAGCGTCGCATGGGCGTGACCACGGTGTATGTGACTCAGATCAGGTCGAGGCCATG
ACCATGGGTGATCGCGTCGCTGTGCTTTTGTCTCGGTGTGCTGCAGCAAGTAGACACCCCG
CAGAACCTGTACGACTACCCAGCAAATGCGTTTCGTGCGCAGCTTCATTGGTTCCCTTCC
ATGAACCTGATTGAGGGCACCATCCGTGGCGATAAGGTCACTTTGGGTACTGGAATTCAG
ATTTCAAGTTCTGATGAGGTGGCAGCAGAGGTTGCAACAACCCGGATCGCTTTGAGGGT
CGTCCAGTCATTGTTGGTGCTCGTCCCAGCACATGTATTTGACCACGGCGAATGAGAGT
GGTGCTGTATTGGGCGAAGTCAGCCACATTGATGAGCTCGGCGCGGATTCATGTTCTAC
GTATTGGCGTCTGGTGTGAAGAACCCGAATACTGATCTTTTGGGTGAGGGCATTCCAGAG
GATATGCGCGTGACCGTTGTGCGGTGCTGAAGAGACCGATAAGGCCCGGCTGGGTATTCGT
GTTGAGCGCCATCACGGTCTGAAGGCCGGCGATAAGGTGCACGTTGTTGCTGCACCGAAG
GATGTTACCTCTTCGACGGTCTTGATGGCGTCGAATCGGTGCATCGGTTCTAGCTCCA
GCCCATACAGTCCAGTCTGGTCAC

>RXN03129-downstream
TAGATTATTTACCAGTGCAACTC

>RXN03164-upstream
CTTTTTTGATCCAGATGCACAAAGCCGTGGCACAAACGAGACAAACTGAGCACAATGGC
TGTCATGGCATATCAACCAGCAGACAATCGCTATGACGAC

>RXN03164
ATGATCTACCGCAGGGTGGGAAATTCTGGGCTGAAGCTTCCGGCAATTTGCTTGGGCTG
TGGCACAACTTCGGTGATGACAAGCCGCTTTCAACGCAGCGCAGCATTATTCACCGCGCG
TTTGATAGGGGAGTCACTCACTTCGATTTGGCTAATAACTATGGACCTCCAGCAGGTTCC

GCAGAGACCAACTTTGGCAGGATTTTGGCTGAGGATCTCAAAAAGCCACCGCGATGAGTTG
 ATCATTTCTTCCAAGGCGGGTTGGGATATGTGGCCTGGACCTTATGGTTTTGGTGGTTCC
 CGAAAGTATCTAGTGAGTTCCCTTGATCAGTCCCTGACTCGCTCGGCTTGGATTACGTG
 GATATTTTCTATCATCACCGCCCGGATCCAGATACTCCTTTGGAAGAAACCATGTACGCA
 TTGCGTGACATTGTTGCGTCTGGAAAGGCTCTTTACGTGGGTATTTCTTCTTACGGTCCA
 GAGCTCACAGCGGAGGCGGCTGAGTTCATGGCGGAGGAGGGCTGCCCCGTTCTGATTTCAT
 CAGCCAAGCTATTTCCATCATTAAATCGTTGGGTGGAGGAACCGGGCGATGACGGTGAGAAC
 TTGTTGCAGTCAGCTGCCAACAATGGTCTTGGCGTCATTGCTTTCTCACCCTTGGCGAG
 GGCCTGCTCACGGACAAATATCTCGATGGAATTCCAGAGGGTTCCCGCGCCAGCCAGGGT
 AAGTCCCTGTCTGAGGGCATGTTGAACGTGAACAATATTGATATGGTCCGCAAGCTCAAT
 GACATCGCCCAGGAACGCGGGCAGTCACTTGCGCAGATGGCGCTTGCATGGGTGCTGCGC
 GAGCAAAGAGAGTACGGCGCCGGATTACCG

>RXN03164-downstream
 TGACCAGTGCATTGATTGGTGCT

RXS00088 - coding Region

ATCGAAGACAACCACGGCACCGAAGGGATCTCCCTGCCAATCGAGGGCGTCGCTGCGACCGACAACCGC
 GCATTGCAACTGCTTGATCGCTGGGGTGTAGAGCTCGTTGCAGCTCCACTTCAGCTGGTTCCATTTACC
 GTTACGGGCTACACCGAAGAGGGCGGCGTCGCTAACCTTGGCTCCCACCGCGAGCCAGACCTGGAAGCA
 CTTGCTGCTGCACAGCCTTCCCTGATCATCAACGGCCAGCGCTTCGCTCAGTACTACGATGACATCATT
 GCCCTGAACCTTGACGCAACCGTTGTTGAGCTAGACCCACGCGATGGCGAGCCACTTGACCAGGAGCTT
 ATCCGCCAGGCTGAAACCCCTCGGTGAGATCTTCCGCGAAGAAGAAGATGCTGCAAAGATCGTTGCTGAT
 TTCGAGTCCGCACTTGAGCGCGCTAAGACCGCATACGCGACAATCTCCGACCAGACCGTCATGGCAGTT
 AACGTTTCCGGCGGAAACATTGGCTACATCGCTCCTTCCGTTGGACGCACCTACGGTCCAATCTTCGAC
 CTGGTTGGACTCACCCACGACTCGAGGTTGGCAACGCGTCCTCCGACCACGAGGGCGACGACATTAAC
 GTCGAAGCAATCGCAGCTGCAAACCCAGACCTGATCCTGGTCATGGACCGCGATGGTGGCACCAGCACC
 CGCAACGAAGCTGATTACGTTCCAGCAGAGCAGATCGTCTCCGACAATGAAGCACTGGCAAACGTCAAG
 GCTGTCACCGACGGATACGTTTACTACGCACCTGCAGATACCTACACCAACGAAAACATCATCACCTAC
 ACCGAGATCCTCAACGGCATGGCAGATATGTTGAGAAGGCAGCTCAG

RXS00088 - 3'-Region
 TAGGGGATCGATCCCACACTGAC

RXS00372 - 5'-Region

GCAGACATTTCCATAAGTCTTGCGAAATGCGCCCATTCATGTAAAGATGTTATTTCTCCCCAAACAC
 TCCTTAAAATTTCAAGAAGGGCCTTATTTTC

RXS00372 - coding Region

ATGTCTTCGAAGCACCCCTTTGAAGCGCACTGCCGTTACTGTTTTTGCACCTCGGCGCTTCCGCTGCTCTC
 CTCGTGGCTTGCTCTGAACCTTCTGAGGACGTTTCCACCGCAGAGACCACCACTGCAAGCTCTTCCGCT
 AACGCATCCGATGCAGCCGGTGAAAAAGTAACCATCACCGTCTACACCTCTGAGCCTGAGGAAAAGGTC
 GATGAGATCAACAAGGCGTTCATGGAAGCCAACCCAGATATTGAGGTTGAGGTGTACCGCGCTGGTACT
 GCGGATCTGACTGCTCGCATTTGAAGCTGAAAAGGCATCCGGTTCTATCGAGGCTGATGTGTTGTGGGCT
 GCGGATGCTGCAACCTTTGAACTTATGCAGCACAGGGCGACCTTGCAGAGCTGGAAGATGTTGAGACT
 TCCGACATCATTGAAGAGGCTCTGGATGCTGAGAAGCTTTTATGTAGGCACCCGCATCATCCCAACCGTG
 ATTGCATACAACACTGAAGTTGTTGATCAGGCTGAGCTTCCCTACGTCTTGGGCTGATCTGACTGATCCT
 AAGTATGCAGGCCAACTGGTCATGCCGATCCAGCTGTGTCTGGTGCTGCAGCCTTCAATGCTTCTGTG
 TGGAAGAACGACCCCTGCGCTTGGCGAAGCCTGGATCACCGCCTTGGGTGAAAACCAACCAATGATCGCT
 CAGTCCAACGGCCCAACCTCCCAGGAGATCGCTGGCGGTGGCCACCCAGTGGGCATCGTGGTGGACTAC
 TTGGTGGCGGACTTGGCTGCTGCTGGATCTCCAATCGACACCATCTACGCATCGGAGGGTTCTCCTTAC
 ATCACTGAGCCTGCAGGTGTGTTGCTGATTCTGAAAAGAAGGAAGCAGCCGAGCGCTACATCAACTTC
 CTGCTGTCTGTTGAAGGCCAGGAAATCGCAGTTGAGCAGGCATACCTGCCAGTGCGTGAAGATGTCGGA
 ACTCCAGAGGGCACCCCCGAGTTGGCTGACATCGAGCTCATGACCCCTGACCTGGAGGTTGTAACCGCT
 GATAAGGCGGCTGCTGTTGAGTTCTTCCAAAACGCAATGAAC

RXS00372 - 3'-Region
 TAGTTTTCTATGCAGTTATCTC

RXS00453 - 5'-Region

TAGTGGGGCGTGAAAAAATAGCTCATTTAAGAGGAGAAGCAACCCCGTGGCGAAATTGCTATTTCAGGTT
GGGGCGATGGTCTATAATCGCAAGTGGATT

RXS00453 - coding Region

GTGATTTTCGGCATGGCTACTTATTTTGGCCATTGTTGGTGGTCTGGCCCTGACGATGCAGAAGGGGTTCT
AGTAACTCTTTCACTAATTGAAGACACCCCTTCGATTGATGCCACTGTTTCTCTGGTTGAAAATTTCCCT
GATCAGACGAACCCGGTGACGGCCGCCGGAGTTAACGTGGTTTTCCAATCCCCGGAAGGAACACGCTT
GATGATCCTCAGATGATGACTGCGATGGATGCAGTCGTTGATTACATTGAGGACAATTTGCCTGATTTT
GGTGGGGGAGAGCGCTTCGGCAATCCTGTTGAGGTGTCTCCTGCGTTGGAAGAGATGGTCATCGAGCAG
ATGACCAGCATGGGGCTTCCTGAGGAAACCGCTGCAAAGGATGCTGCCAATCTGGCGGTGTTGAGCGAA
GACAAAACCATTTGGCTACACCTCTTTCAACATTGATGTTGAGGCCGAGAAATATGTGGAGCAAAAACAC
CGCGATGTGATCAACGAAGCGATGCAAATCGGTGAAGATTTAGGTGTCCGGGTGGAAGCCGGTGGACCT
GCTTTCGGTGATCCAATTGAGATTGAAACCACAGTGAGATCATCGGTATTGGCATCGCGTTCATCGTG
TTGATTTTCACCTTTGGTTCTTTGATTGCTGCAGGCTTGCTTTGATTACCGCGGTGATCGGCGTGGGC
ATTTGGTGCCTGGCAATTGTGCTGGCCACGGCGTTTACTGATCTCAACAATGTGACTCCAGTGCTCGCA
GTGATGATTGGCCTGGCCGTGGGCATTGACTACGCGCTGTTTATTTTGTCTAGGTACCGTGCGGAGTAT
AAGCGCATGCCACGTGCCGATGCTGCCGGAATGGCGGTGGGCACAGCTGGTAGTGCGGTGGTGTGCT
GGCGCGACGGTGATTATCGCGCTGGTAGCCCTCATCATTGCGGATATCGGATTCCTCACGGCCATGGGT
ATTTCTGCGGCGTTTACGGTGTTCTGCTGCTCATTTGCGTTGACGTTTATCCCGGCGCTGTTGGGT
GTGTTTGGTGGTCATGCGTTCAAGGGCAAGATCCCTGGAATTGGTGGAAACCCAAACGCCAAAGCAGACG
TGGGAGCAAGCGCTTAATCGTCGTTCCAAGGGTCGCTCATGGGTCAAGCTTGACAGAAAGCACCGGGT
CTTGCTGGTGAGTGGTGGTCTTGGGTCTTGGTGCTTGACCATTCCTGCAATGAACCTGCAGTTGTCA
CTGCCTTCTGACTCCACCTCCAATATTGATACCACTCAGCGTCAGTCGGCTGATTTGATGGCAGAGGGC
TTTGGCGCGGGCGTTAATGCGCGCTTCTTGGTCATCGTCGATACGCATGAGGTCAATGCTGATTCCACC
GCATTGCAGCCACTGATTGAGGCACAGGAGCCTGAAGAGGGCGAGTTCGATCGGGAGCAGGCGGCTCGT
TTTGCTACCTATATGTATGTACCCAGACCTACAATTCCAACATCGATGTGAAGAATGCGCAGATCATC
AGCGTCAATGATGATTTCACTGCGGCGCAGATTCTCGTGACTCCATACACCGGACCTGCGGATAAAGAG
ACCCCTGAGTTGATGCACGTGCTGCGTGCGCAGGAAGCTCAGATTGAGGATGTTACGGGAACCTGAACCTG
GGTACCACTGGGTTTACGGCGGTTTCACTTGGACATTACTGAGCAGCTGGAAGACGCAATGCCGGTTTAC
CTCGCTGTGGTGTGTTGGTTTGGCTATTTTCTCTCCTCATTCTGGTGTTCGGTTCCCTGCTTGTTCGCTG
GTTGCTGGCCTTGGCTTCTTGTGTGCTGTGGGTGCGGCCTTCGGTGCGACGGTGTTGGTCTGGCAGGAG
GGCTTCGGTGCTTTGTGAACACCCCTGGTCCGCTGATTTTCTTCATGCCGATCTTCTCATCGGCGTG
ACCTTCGGTTTGGCCATGGACTATCAGGTGTTCTTGTGACTCGCATGCGCGAGCACTACACCCACCAC
AATGGCAAGGGACAGCCTGGTTCCAAGTACACCCCGGTTGAGCAGTCAGTGATTGAAGGCTTCACGCAG
GGTCCCGCGTGGTTACAGCAGCGGCACATGATGATTGCCGTGTTCTGTTGGCTTTATTGATCAGCCG
TTGCCATTTATTAAGATCTTCGGTTTCGCGTTGGGTGCGGGCGTGTTTTTCGATGCTTTCTTCATTTCGC
ATGGGTCTGGTCCCCGCGTCGATGTTCTGATGGGCAAGGCCACGTGGTGGATGCCTAAGTGGCTGGAT
CGAATTCTGCCAAGTTTGACATTGAAGGCACCGCACTGGAGAAGGAATGGGAGGAGAAGCAGGCTGCA
CGT

RXS00453 - 3'-Region

TAGACTTGGCACCTATGTCAGAT

RXS00479 - 5'-Region

TAGATCCCAAGGCTCAAAATTTATTACTTAAACAAGTTGAGCAACTAGCCAGCCGCAAATCTTAGAACT
AACCTTTACGCCTTTAACGGAAGTGAATTTG

RXS00479 - coding Region

ATGTCTACTAGCATCACAAACAGAGAACAAGAAGAAATCTGGTCCTCCTCGCTTGATGAGAATCTTTCTG
CCCGCCTTGCTAATTTTAGTTTGGCTTGTAGGAGCTGGAGTCGGCGGTCCTTATTTTGGCAAGGTTAGT
GAGGTCTCCTCCAACAGCCAGACCACATATCTGCCAGAATCTGCCGATGCCACTCAAGTACAGGAACAG
TTGGGAGATTTTACTGATTCTGAATCCATCCAGCCATTGTGTAATGGTCAGCGATGAACCTTAAACA
CAGCAAGACATCACACAACCTCAATGAAGTTGTTGCTGGGCTTTCAGAATTAGACATAGTTTCCGATGAA
GTCTCCCTGCTATTCCATCCGAGGACGGCAGAGCTGTCCAAGTGTGTTGTCCTTCAATCCATCAGCG
GAGCTGACGGAAAGCGTCGAGAAGCTCTCTGAGACCTTGACCCAGCAAACGCCGGACTATGTGAGCACC
TATGTGACCGGACCGGCTGGGTTTACCGCTGATCTCAGCGCAGCTTTCGCGGGTATTGATGGGCTACTC
CTAGCAGTCGCCTTGGCTGCCGTCTTGTCACTTCTGTCATCGTCTATCGCTCCTTCACTTCTGCCATC
GCCGTGCTTGCCACCAGTTTGTGTTGCGCTGACTGTAGCTCTATTGGTGGTGGTGGTGGCTAAGTGG
GACATCCTGCTGCTTTCGGGTCAGACTCAAGGCATCCTCTTCATTCTGGTCATTGGCGCCGCCACCAC
TACTCATTGCTATACGTTGCTCGTTTCCGTGAAGAGTTACGCGTTCAACAAGATAAAGGGATAGCCACA
GGGAAAGCCATCCGGGCATCGGTGGAACCCATTCTTGCTCGGCGAGCACTGTTATTGCGGGCCTCCTT

TGTTTGCTATTTAGTGATTTGAAATCTAACTCCACGCTAGGTCCAGTAGCTTCGGTGGGCATTATTTTT
 GCAATGCTTTCTGCTCTTACTCTGCTACCAGCCCTGCTGTTTGTATTTCGGTTCGGGTGGCCTTTTGGCCC
 AAGCGACCAAAATACGAACCTGAAAAAGCCCGTGCGAAAAACGACATCCCCGCCAGCGGGATCTGGTCA
 AAAGTGGCTGATTTAGTGGAGCAGCATCCTCGTGCAATCTGGGTATCTACACTTATTGTGCTTCTCTTG
 GGTGCGGCTTTTCGTTCCACACTAAAAGCGGACGGTGTGTCCCAATCCGACCTAGTTCTGGGTTCCTCT
 GAAGCAGTGATGGCCAGCAGGCTTTAGGCGAACACTTCCCCGGTGGATCCGGCAGTCCTGCTTATATT
 ATCGTTGATGAAACACAGGCAGCACAGGCTGCTGACGTAGTCCCTAACACGACAATTTTCGAGACTGTA
 ACTGTAAGTAGTGCTGACTCCCCCTCTGGCTCAGCCCCAATCACCGCTGACGGTATTGTGCCGTTAGGT
 TCTGGTACAGCTCCAGGCCCGGTAGTTGTAGAAGGGCAAGTCCCTTTACAAGCAACACTTGTCTGAAGCA
 CCAGATTCCGAAGAAGCTCAAAAAGCTATTTCGCAGTATCCGCCAAACTTTTGCAGATGAAAATATATCA
 GCGGTAGTAGGCGGTGTCACTGCAACTTCCGTAGACACTAACGATGCCTCCATCCATGACCGCAACCTG
 ATCATCCCAATTGTATTGCTGGTCATTTTGGTTATTCTCATGCTGTTGCTGCGGTCTATTGTCTGCACCA
 CTCCTGCTAGTAGTCACCACCGTGGTGTCTTTTGTCTACTGCTTTAGGCGTGGCTGCTTTACTTTTCAAT
 CACGTTTTTCAGTTTCCCAGGAGCAGACCCCGCAGTACCTCTCTACGGATTTGTATTTTTAGTAGCCTTG
 GGCATCGACTACAACATTTTCTTAGTCACCCGAATCCGTGAAGAAACCAAAACCCACGGCACAAGACTT
 GGAATTCTTCGAGGCCTGACAGTAACCGGCGGAGTAATTACCTCAGCTGGAGTAGTTCTCGCCGCAACG
 TTCGCAGCACTCTATGTCATCCCAATTCTATTTCCTGGCACAATTCCTTCATTGTCTGCTTTTGGAGTT
 CTTATTGATACCTGCTCGTTCGCGCCTTCTTGGTGCCTGCTTTGTTCTACGACATCGGACCGAAAATC
 TGGTGGCCGTCAAAATTGTCCAATCAGAAATACCAGAAGCAGCCTCAGCTA

RXS00479 - 3'-Region
 TGACACACCAAAATTCGCCTCTC

RXS00654 - 5'-Region
 CAGCAATAGCGATTATTGCTTGATTGTGTGTTTTTAGATCTTCGGTCTCTTCACTCAACTGCTGTGAA
 GTGCCACCTGTTTGAAAGGCGAACACGATA

RXS00654 - coding Region
 GTGCTCGATATTTTGATTACCCGGTGTCTGGAGTGATGAAGCTGTGGCACCTGCTTCTTCACAACGTT
 GCGGGTTTGGACGATTCACTGGCGTGGTTCTTTTCCCTTTTCGGCCTTGTCATCACGATCCGTGCAATT
 ATCGCGCCTTTCACTGGCAGATGTATAAGTCGGGCGCAGTCCCGCACATATTCGTCTCACCAGCGCT
 GCGCTCCGGGAAGAATACAAGGGAAGTACGATGAAGCGTCCATTTCGGGAGTTGCAGAAGCGCCAGAAT
 GATTTGAATAAGGAATACGGCATTAAACCCGCTGGCAGGTTGTGTGCCTGGGCTGATCCAGATACCGATT
 GTCCTTGGTCTTTACTGGGCATTCTCCGCATGGCTCGCCCTGAAGGTGGTTTGGAATATCCCGTCTTC
 CAGTCGATCGGCTTCTAACTCCTGAGGAAGTGAATCTTTCTCGCTGGTTCGCGTGAGCAATGTGCCT
 CTGCCCGCTTATGTTTCGATGCCCCACTGAGCAGCTAAAATATTTGAGCACCCACGCAGGCGGAAGTTCTT
 AGTTTCGTTTTTGCCACTGTTTCATCACAGCCGCAATCCTCACCGCAATCAACATGGCGATGTCCATGTAC
 CGCAGCTTCCAAACCAACGATTACGCATCCGATTCTCTAACGGCATGCTGAAGTTCATGATCGTGATG
 TCGATCCTCGCGCCGATCTTCCCACTGTCCCTTGGCCTCACAGGACCATTCCCCACGCAATCGCACTC
 TATTGGGTGAGCAACAACCTGTGGACGCTCCTCCAAACAATCATCATGATGGTCAATTTGGAACGCAAA
 TACCCACTTACCGACGATTTCAAAGTGACACCTAGAGCAGCGCGACATCTACCGCGCAAAACAAAA
 GAAAAGCGCATCTTCTGTGGACACGACGCAAAACCGCGCCCTGATGATTCTACCCCATGGAACGCC
 TCAACGCTTACGCAACAACGTGGAATCACCAAAACCCGTACTGCCGAAATCAACGAAGCAAAACAG
 GCCCGCAAAGAAATCGCAACAAGAGGCGCAACGCAACGTGAAATGAACCGCGCCGATGCAGCGC
 TTAAAGCAGCGTCGCGCTGAGGTAAAGCTAAAAAGAAGGGCTTATCGACGCCTCCCCAACGAAGAT
 ACCCCTTCGGAATGAAGAACTAAATTGAGTAGTCCGCAGGTGGAGCCGACAACAACTGCCGAGCCA
 AATCGCGAGCCGTCTCAAGAGGAC

RXS00654 - 3'-Region
 TGATGTTGTGGACCAATCGAGAT

RXS00758 - 5'-Region
 TTCAAGTTTGGCTGTGACTCATGTGCGACATAGTATTTCAATCACCGGATCCGCACGATTGCAAAATCC
 TGGGGAATATTACATAACAACGGAGGTCACTC

RXS00758 - coding Region
 ATGACTTTGAAGAAGTCTCTCGCTGTAAACCACGGCGGCTGCACTTGCTTTGAGCCTTGCCGCTTGCTCG
 TCCGACTCCTCGTCCGACAGCTCCTCATCTCATCAGGCAGCGAAGGCGGCGACAACCTACGTCTCTCGTC
 AACGGCACTGAGCCACAGAACCCGCTCGTCCCAGGCAACACCAACGAAGTAGGTGGCGGTGCGCATCGTC
 GACAGCATCTTCTCCGGCCTGGTCTACTACGACGTGACGGCTCCCCTGTCAACGATGTTGCAGAGTCC
 ATCGAATCGAAGGTGACAAGACCTACCGCATCACCATCAAAGACGGCCAGACCTTACCGATGGCACC

CCAGTTACCGCTGAGAGCTTTGTCAACGCATGGAACATAACGTAGCTAACAGCACGCTGTCCTCCTAC
 TTCTTTGAGTCCATCCTCGGCTACGAAGAAGGCGTCGAGTCCATGGAAGGCTCCAGGTCGTCGACGAC
 ACCACCTTACCGCTCGAGCTCACCAGCCTGAGTCCGACTTCCCACTGCGCCTGGGATACTCCGCATTTC
 TTCCCGCTTCTGAATCCGCATTTGACGACATGGACGCATTTCGGTGAGAACCAATCGGCAACGGTCCA
 TACAAGCTCCAAGAGTGGAACCACAACCAGGACGCCACCATCGTTCTTAACGCGGACTACACCGGTGGA
 CGCCAGGCTCAGAACGACGGCGTGAAGTTCATCTTCTACCCAACCTTCGACTCCGCTTACGCGGACCTG
 CTCTCCGACAACCTTGATGTGCTGGACGCTATCCCAGACTCCGCGTTCTCCTCCTTCGAGGACGAGCTC
 TCTGGCCGTTCCATCAACCAGCCTTCCGCTGTGTTCCAGTCCCTTACCATCCCGGAGAGCCTTGAGCAC
 TTCTCCGGCGAAGAAGGCGTGCTGCGTCGCCAGGCCATCTCCTTGCCGCTCAACCGCGACGAGATCACC
 CAAACCATCTTGAAGGCACCCGCACCCAGCGACGGAAGTTCACCTCCCCTGTCATCGACGGACACTCT
 GATTCCCTCCAGGGCGCAGATGTCTTGACCTACGATCCAGAGCGCGCTCAGGAAGTGTGGGCACAGGCA
 GACGAGATCAGCCCTTGGTCCGGCGAGTTCTCCATCTCCTACAACGCAGACGGTGGACACCAGGCATGG
 GTGGACGCAACCGCCAATTCCATCCGCAACACCCTGGGTATCGACGCCATCGGCAACCCATACCCAGAC
 TTCAAGTCCCTGCGTGACGATGTACCAACCGCACCATCAACGGCGCATTCGCAACCGGCTGGCAGGCA
 GACTACCCGTCCTTGGGCAACTTCTCGGACCTTTGTACGGCACCGGTGCAGGCTCCAACGATGGTGAC
 TACTCCAACCCAGATTTGATGCCAAGCTCGCCGAAGCAGCAAACGCGGCCGATGTTGACGCATCAACC
 CCGCTATAACAAGCAGACAGGAAATCCTGCTCCAGGATCTCCAGCGATCCCAACTTGGTACTCCAAC
 GCAGTTGGTGGATACTCCACCAACGTGGACAACGTGGAATTCAGTGGAAGTCCGAACCTGCGTACTAC
 CAGATCACCAAGAAC

RXS00758 - 3'-Region
 TAGTAGCTTCGCACCAACCGCTC

RXS00912 - 5'-Region
 CCACACCTTTGAAAGGAGCTAAGCG

RXS00912 - coding Region
 ATGGACAACACCTCTACACAGCAGGCCCTACAATCGCAGCTGCCTTTTTTCATGCTGTCGTTTCATCTTC
 ACCATCTACCGCATCATCGTCGGGCCCCAATCCATCGATCGCCTACTCGGCCTGGACGGAACCGTCTCC
 ATGATTCAATGCTCCATGGCCACCTACATCTGCTGGACACTCGACACCACCGTCACCAACTTCATGATG
 GTCATCGCACTCTTAGGATTCATCAGCTCTGTATCCGTAGCCCGCTTCCGCAAGAGGGATGGTGCC

RXS00912 - 3'-Region
 TAAATGACCCTGCAACTATTCAC

RXS00932 - 5'-Region
 CCCAATTAATTTATGCACTTCGGTGAGGTTACTCACAAAGAGTAGCGTGCAAAGCCCAGCAATAAGGTG
 ATGTTTCAACGATTAGGTTACGGTAGGGGCC

RXS00932 - coding Region
 ATGACGCCACAGAACTTCACCGTTTTGTCAGCCCTTTTAGAAATGGGTACCTGGACCCTGCTGATCATC
 GGCATGATCTTAAAATACAGTGGAGTGACAGACGCCGTAACCCCTATTGCCGGCGGTATCCACGGCTTT
 GGCTTCTCTGTTTTGCAGCCATCACCATACCGTGTGGATCAATAATAAGTGGACATTCCCGCAGGGT
 ATCGCAGGTTTGATCGTCTCTGTTATCCCGTGGGCTGCATTGCCATTTGCATTGTGGGCAGACAAGAAG
 GGCCTCGTTGCCGGCGGATGGCGCTTTTCAGATCCGTCCGAAAAGCCACACACTTTCTTTGACAAGATC
 TTGGCTCAATTGGTCAGGCACCCAATCCGATCCATTTAATTCTGCTGGTGATTATCGCCGTCGTCTTC
 TCTATCTTGCTGGCGATGGGACCACCTTATGATCCAGATGCCATCGCAAACACTGTGGAT

RXS00932 - 3'-Region
 TAAACAACAGCCTCCTTCACATG

RXS01346 - 5'-Region
 AAGGTGTGGTGAGTCACTGGCTAGATTTGATTTGTTGGCCATACCAAATCGGCCCCACACAGGCACGTTG
 CAAACAGCAACGCTCACCCATAGGAGATTTA

RXS01346 - coding Region
 ATGCGCACAGCCACAAAAGTCACGCAACAGTGATGGCCTCAACCCTGGCTATCGGGCTGGCATCTTGT
 TCCAGCTCTAGTGGCACCCAGCGTGAATTACGTATCCGTCAACGGCACCGAACCTCAGCGCGGACTC
 ATCCCGGGCGACACCAATGAAAACGGCGGTGGGCGAGTGGTGGACATGCTGTACTCTGGGCTCGTCTAC
 TTTGATGAAGCTGGCGTTGCTCAAAATGACCTGGCGGCATCAATTGACCAGGAAACAGACACCACCTAC
 AAAATCACTTTGCGTGATGGCATCAAATTCAGTGACGGATCGGATATTACTGCCACTGATTTTGTGGAT

ACCTGGAATTTTGTAGTGAAAAATGGACTGCTCAACACTTCTTTCTCTCACCGATTAAAGGGTATGAG
 GAGGGCGTGGAACGCTCGAGGGTTTGAATGTGGTGGATGATCGCACATTTACCATCGAGCTTGCCCAA
 CCGGATTTCTGAGTTTACCCACGCAATGGCTACTACGGTTTTCACCGATGCCAGCTTCGGCTCGCGAT
 GATATTGACGCCTTTGGTGAAAACCCCGTGCTCTGGCCCTTACAACTAGAGCAGTGGGATCACAAC
 GCAGAACTGAAAGTGGTGGCCAATGAACACTACGATGGCCCGCGCGCAGCCAACAACGATGGCTTGAAG
 TACGTGTTCTACGCCCCAAAATGATGCAGCTTATTAGATCTGTTGGCTGGAAACCTAGATGTGCTGGAT
 CTCATTCCACCATCGGCGTACACCACCTATGAAGAGGAACTGTCGGGTCGATCCATTAATCAACCTGCG
 GCCTCCTATCTGGAACCTCTCATTTCGCATGGAATCCCCCACTTTGAAGGGCAACAGGGACAGTTGCGT
 CGACAAGCAATTTCTATGGCGATTAAACCGTGAAGAAAATCGCTGAGCAGATCTTCGCCGGCACCTACACG
 CCTGCGCTCGACTTCACCGCGCCCGTGCTCGACGGCTGGCGCGATGATTGAACGGCAATGACGTGCTG
 ACTTTCAGCCTGACAAGGCCCGTGAGCTGTGGGAAGACGCTGAGGAGATCGCACCTTTTGAGGGCGAA
 TTGCAGATCAGTTACAACGCGGATGTTCCCAACCGGAATGGGTGGATGCGGTGACAAACATCAGC
 AACGAATTAGACGTCAACGCCACTGGCAATCCTTTCCCGATTTTAAATCCTTCGCGACACATACCGC
 ACCACCGGATTGGATGGCGCCTACCGCACCGCTGGTTTGGCGACTACCCAAGCATCGGCAACTTCCTT
 GGACCTAACTACACCTCGGGCGTGGCCTCCAACGATGCCAAGTACGAAAACCCAGAATTTGATCAATTG
 ATTGCCGACGCCGAGCAGCCTCCACCAAGGAGGAAACCTTCCAGGCATATGCGCAGGCCCAGGAAATG
 TTGTTGCGCGATCTTCCCGCAATCCCACTGTGGTACCCGAATGTGGTTGGCGGCTACTCAGAATCCGTG
 GACAACGTCTCCGTAAACTGGAAGGCCATACCTGTTTATTGGGCAATTACAAAGCAA

RXS01346 - 3'-Region
 TAAACTCATTAACCTAAATCCGG

RXS01425 - 5'-Region
 AGTCCCTATTAATCCCAAGGAGTTTCGACTCACAGTGCTCAATTTTATTATTGGCCAATTTTCGGCCAT
 TCTGTGGTTCTGGCATAAAGCGTTTCAGCTTT

RXS01425 - coding Region
 GTGCTGAGCCAGATTCCGGAATTACCTGGGCTTGTGCGATCATGTTCTTGACCTTCACCGTGCGTATG
 GTTCTGGTCAAGCCGATGGTCAACACCATGCGTTTCACAGCGCAAGATGCAAGACATGGCTCCAAAGATG
 CAGGCCATCCGCGAGAGTACAAAAATGACCAGCAGAAGATGATGGAGGAGACCCGCAAACTTCAAAAA
 GAAGTGGGCGTTAACCCCATCGCAGGCTGTTTGCCAATGTTGGTGCAGATCCAGTGTTCTCTGGGTCTG
 TTCCACGTGCTGCGCTCCTTCAACCGCACCGGTTCTGGCGTTGGCCAGCTGGAAATGACCGTTGAGCAA
 AACGCGAACACCCCGAACTACATCTTCGGTGTGACGAGGTTTCAGTCCTTCTGCGTGCAGACCTGTTT
 GGTGCGCCACTGTCGTCCTACATCACCATGCCTGCTGACGCGTTCGACGCGTTCCTTGGCCTGGATGTC
 TCCCGCCTCAACATCGCGCTGGTTGCAGCTCCAATGATTTTGATCATTTGTCGTGGCAACTCACATGAAC
 GCGCGTCTGTCCGTCAACCGCCAGGAAGCTCGCAAGGCAGCCGGCAAGCAGCAGGCCGCTTCCAGCGAT
 CAGATGGCCATGCAGATGCAAATGATGAACAAGATGATGCTCTGGTTTCATGCCAGCCACCATTTTGTTC
 ACCGGCTTCATCTGGACCATCGGTCTTCTTGTCTACATGATGTCCAACAACGTGTGGACCTTCTTCCAG
 CAGCGCTACATCTTCGCCAAGATGGACGCTGAGGAAGCAGCTGAGGAGGAGGAAAAGCGCGCAGCAAAG
 CGCACTACCGCTCCAAAGCCTGGCGTGAAGCCAGAAAACCCCAAGAAGCGTAAGAAG

RXS01425 - 3'-Region
 TAAAACTTCACTAAAAACCGCCA

RXS01658 - coding Region
 GATCCACAGATCCTGTACCAACCTTCACCCAGCAACAGCAGCTGCGAACTTCTACGGTTTCCAGAGC
 CAGCTGGCGATGGACCGCTTTGAAGTAGATGGCAAACCTCCGCGACTTTGTTGTGGCAGCACGTGAGCTC
 GATCCAAACGCCCTGCAGCAAAAACAGCAGGACTGGATTAACCGTCACACTGTTTATACCCACGGCAAC
 GGCTTCATTGCAGCTCAAGCAAACAGGTGGATGAGGTGCGCCGCGACGTCGGATCCACTCGTGGTGGT
 TACCCTGTCTACACCGTCTCTGATTTGCAGTCAATGCTCGTGTGCTGCAGAAAGCGAAGATGCTGAGGAG
 CTTGGCATCAAGGTTGATGAGCCTCGTGTGTACTACGGACCACTGATTGCTTCTGCGACTGATGGTGCT
 GACTACGCAATTGTGCGGTGACACCGCGATGGCCAGTCGAGTACGACACTGACACCTCCAGCTACACC
 TACGAAGGTGCTGGCGGCGTGGACATTGGAACATGGTCAACCGTGCGATGTTTGCATTGCGCTACCAG
 GAAATGAACATGCTCCTGTCTGATCGTGTGGTTCCGAATCCAAGATCCTATTTGAGCGCGATCCTCGT
 TCCCGTGTGGAAGGTTGCACCTTGGTTGACCACTGACTCCAAGACCTACCCAACCTGTGATTGATGGT
 CGCATCAAGTGGATCGTCGATGGCTACACCACCTTGGATAGTCTTCCGTACTCCACGCGACCTCACTG
 ACGGAAGCGACTCAGGATGCTGTATGCCTGACGGCACCCACAGCCACTGATCACAGATAGGGTGGT
 TACATCCGCAACTCCGTGAAGGCTGTTGTTGATGCGTACGACGGAACGTTGAACCTTACGAATTTCGAC
 ACCGAAGATCCTGTTCTGAAGGCATGGCGTGGCGTGTTCAGACACCGTGAAGGACGGGTGCGGAGATT
 TCCGATGAGCTTCGCGCACACCTGCGTTACCCAGAAGATTTGTTCAAGGTCCAGCGTGACATGCTGGCC
 AAGTACAACGTTGATGATTCTGGAACATTCTTACCAACGATGCGTCTGTTCTGCTCCAGGTGACCCA

ACTGCAGCGGAGGGCCGCCAGGAACCTTAAGCAGCCTCCTTACTACGTGGTGGCAGCAGACCCAGAGACC
GGTGAGTCCAGCTTCCAGCTGATCACCCCGTTCCGTGGACTTCAGCGCGAGTACCTCTCTGCACACATG
TCTGCGTCTGCTGATCCAGTTACCTACGGTGAATCACTGTTTCGTGTGCTGCCTACCGATTCTGTGACC
CAGGGTCCAAAGCAGGCCCAGGATGCGATGATGTCATCTGACCAGGTTGCTCAGGACCAAACACTGTGG
CGTGGATCGAACGATCTGCACAACGGAACCTGTTGACCTTGCCAGTTGGTGGCGGAGAGATCCTCTAC
GTTGAGCCGATTTACTCGCAGCGCAAGGATCAGGCATCGGCCTTCCCGAAGCTTCTGCGCGTGTGGTC
TTCTACAAGGGTCAGGTTGGTTACGCACCAACGATCGCTGAAGCCCTATCGCAGGTCGGCATTGATCCG
AAGGAAGCGCAGGACATCGAAGAGGTAGATGGCACCCTACGACGCCATCGACTGATGAGACTGACACT
GACACTGATCAGCCTGCAACCGAAACCCCAACTGCACCAGTGAGTGAGGCGGAAGGAATCGCGGCCATC
AACGATGCGTTGAGCAACCTTGAAGCTGCTCGCGATAGCTCTTTCGAAGAGTATGGTCTGCACTCGAT
GCGCTTGATCGTGCCGTCGATAGCTACCAGTCCGCACAG

RXS01658 - 3'-Region
TAGCGTTTGAGTAAACAGCCCGA

RXS01677 - 5'-Region
GTCGCCATAGTTGAGTTTTATTTCATGGCTTTTAGCTAGGCGACTTTAGTTGAGGGCTTTTAGTTGAGGG
CTTCCCAGCAGGGATGTTAAGGAGAATTCA

RXS01677 - coding Region
GTGAACCAACAGAGTAAAAAGTGGCTCGTACCGACACTGGTTCGTTCATCATTGCAGTGCTCCTCATCGCA
GTTGTTCTGTTGATGTACCGAGGAAATGCGAGTGATACGGCCGAGGGCGTTTCAGCCGCTGCGACTTCG
GACTCGGCTGCTGCTTCGACTGCTGCTTCGGGTTCCGCTTCTGGTGTGCGGACTCCGATCTGACCAGC
GTGGAAGCACGCGACCCCTTCGACCCCTGTTGCGGTGGGAGACGTTGATGCACCTGTTGGGTAGTGGTG
TTTTCCGACTACCAATGCCCCGTTCTGTGCAAAGTGGAGCGATGAAACCTGCCACAGATGATGAAGCAT
GTGGAAGATGGAACCTCCGCATTGAATGGCGTGAAGTGAACATCTTTGGAGAACCATCTGAGCGTGGA
GCTCGCGCGGCATACGCTGCGGTTTTGCAGGACGCATACTTGAATACCACAACGCACTCTTTGCCAAC
GGTGA AAAACCCAGCGAAGACCTGCTCAGCGAAGAGGGACTTATTAAGCTTGCTGGTGACCTTGACTA
GACGAATCGAAATTCATGCCGATTTCCAATCCCCTGAAACTGCAGTCGCAATTGCGCAACATCAACAG
CTGGGAATCGATCTTGCGCCTACTCCACCCAGCTTTCTCTCTAGGTGGCCAGCCAATCATGGGCGCT
CAGCCTGCTTCTGTATTTGAAGCCGCTTCGAGCAAGCACTGGCAGCGAAAGAA

RXS01677 - 3'-Region
TAAACCGTGGATGTCGGCCTAGT

RXS02586 - 5'-Region
TTCTCTGAGATCGTCATGATGAAGTACATCGCGTTCGGCATGATCGCAGCGCTGATTCTGGATGCCACC
ATCATCCGCATGCTGCTTGTCCTCCCGCCGCTG

RXS02586 - coding Region
ATGCACCTGCTTCGCGACGACAACCTGGTGGGCACCCGGCTTCGTTAAAAAGGCCCTACACCGTCATGGGT
CACGGCTCTGAGGTGGAGGAAGCACCTCGCCCAACACCCGTCGCCTCAACGACGATGAGGAAGTCACC
GTGCATGAAGCAGTTGTGCTGCGGATACCGTGGCATCTCGCGGTGGTTGAGCACGCAGGAAAACCGT
GATCTGGTGTCTTCGTGGAACCTAAGGCTCGTTTGAAAAGCGCAGGCTTGAGGATCTAGAT

RXS02586 - 3'-Region
TAAATCTATGCGAGGATTTTTCA

RXS02587 - 5'-Region
AGCCTGGATAACCTGCCAGACGGTGGCGCATGGCTGCAGCCGTTCCGCCCTCTGACTGCCTTGTTATCC
AACCGCCACAATTCCCAGGAGTAATCCACCC

RXS02587 - coding Region
GTGTTTTCTAAATGGGGCCACTTTGCTTACAGATTTAGGCGCATTTGTTCCGTTAGTCGTCATCGCCGCG
ATTTTGCTTTGTTTGTGATTTTCGGCACCAAGCTGGGCGACCGCATGAGCCAGGAAGGATGGGATGAT
CCTGTTCTTCTCGACCGCTGCGGCGGCATCGAGTTGGAGACCTTTGGGCGTGACAATGACGGCGAT
GTCGTGTTGCTGTTTACTGCGCCTGAAGGCATTTCTTTCGATGATGCAGAGGTGTTCTCCAGCATCTCT
GGCTACTTAGATGGGCTAATCGAGAACAACCCCTGATGAAGTCAGCCACATCAACAGCTACTTTGACACT
CGTAATCAAAATCTCCTCAGCAAAGACGGCACCCAAACCTTTGCAGCTCTCGGGCTCAAAGGTGACGGC
GAGCAAACGCTGAAGGACTTCCGGGAGATTGAAGATCAGCTCCATCCGACAACTTGCCGGTGGCGTC
ACCACTGAGGTGCGGGGTGCCACCGCTGTAGCCGACGCACTCGATGAGGGCATGGCTGGCGATATTTCA

CGCGCCGAAGTTTTTGCCTGCTTTTCGTGGCTATCTTGCTGCTCATCGTGTTTGGCTCAGTTGTTGCC
GCGGCGATGCCATTGATCGTGGGCATTTTGTCCATCTTGGGTTTCGCTGGGCATCTTGGCAATTTTGGCT
GGATTCTTCCAGGTCAACGTATTTGCACAATCTGTTGTGACCCCTTCTGGGCTTGGGTCTTGCCATTGAC
TATGGCTTATTCATGGTCTCTCGTTTCCGTGAGGAAATGGATAAGGGCACCCCGGTTGAACAGGCTGTT
GCCACCACTACGGCGACCGCGGGTAAGACTGTGGTGTCTCTGCAGCGATGGTGGCTGTGGCGCTGTCC
GGGTTGTTTGTGTTTTCCACAGGCTTTCTTGAAGTCGGTGGCATTCGGTGCGATTTCGCGGGTTGGCCTT
GCTGCTTTGATGTCGGTGACGGTGTGCGCTCGCTGTTTCAGCATGTTGGGTAAGAATATCGATAAGTGG
AGTTTGCCTGCGCACTGCTCGAACAGCGCGCCGTTTGGAGACACCATTGTTGTTACCGCTGCCGGCATGG
GCAATGCGCCATGCCAAGGCAGTGACCGTGGGCGTCGTATTGCTCTTGCTTCTTACAGTGCCGTTG
ACGGGCGTGAAATTCGGCGGCATCAATGAAACGTATCTGCCACCAGCTAACGACACCCGCGTCGCCCAA
GAGCGTTTCGACGAGGCGTTTCCCGCCTTCCGCACCGAGCCGTCAGCTTGTGGTCACCGGGGCGGAC
AACAACCAGCTGATCGATATCTATGTTTCAGGCCAACGAAGTTGAGGGACTGACAGATCGTTTACCCGCA
GGTGGGACTACCGATGATGGCACCACGGTGTGTCTACTGGTATTTCAGGATCGTTCCCTCAATGAGCAG
GTAGTGGAGCAGCTTCGCGCTATTTCCGTCCCTGAGGGCGTTGAGGTGCAGATCGGTGGCACTCCAGCC
ATGGAGATCGAATCCATTGAGGCGCTCTTTGAAAAGCTCCTCTGGATGGCTCTCATATTGTGCTGGCC
ACTTTCATCCTCATGGCATTGGTATTTGGTTCGGTGATTTTGGCGGCGAAGGCCATCATCATGACCATT
CTGGGTATGGGTGCCACCTTGGGTATTCTCACCTTGATGTTTCGTCGATGGCGTGGGTGCCAGCGCATTG
AACTTCTCCCTTGCCCACTGATGAGTCCAGTGCTGGTGCTGATCATGGCTATTATTTACGGACTTTCC
ACCGACTATGAGGTGTTCTTGGTATCTCGCATGGTGGAGGCCCGGATAAAGGCGAATCCACCGACGAC
GCCATCAGATACGGCACTGCACACACCGGATCTATCATCACCGCGCGCGCACTGATCATGATTGTGGTC
TGTGGAGCGTTTGGTTTCTCTGAGATCGTCATGATGAAGTACATCGCGTTCGGCATGATCGCAGCGCTG
ATTCTGGATGCCACCATCATCCGCATGCTGCTTGTCCCCCGCGTGATGCACCTGCTTCGCGACGACAA
CTGGTGGGCACCCGGCTTCGT

RXS02587 - 3'-Region
TAAAAAGGCCTACACCGTCATGG

RXS02590 - 5'-Region
GCCCCAAAGGCTTAAAGTAATGGGCATGCCCACTCCTTCTTCGACCAAAAGCTACGCTGCGGTCTTACC
TCCACCTGGCCCCCTCGTGGGCTGGTTCCCTC

RXS02590 - coding Region
ATGGGCATCTCATTGTTGTCATCACTGTTGAAAATCCATGGTTTTCCAGTCGTCGCAGATTTCTTCTTC
GCGTTAGCTGTTGTGGTGGCAATTGTCAATTATTGGCGGTTGGCTAATCTACCGCTCTCCTTCATTCAAA
ACTGAAGTCATGCCGGCATGGGCAATGCTGTCCATGGGTTTGATCGCATGGGAACTGCAAGCCCCGTA
GTTTTGGGTGATGATCTGTGGGATTTATGTTTGTGTGCTGGTCTATTGGCACAGCCGTGGGACTTGTT
GCCTATTCCTTATATATAACGGCCATTTTGCGATCTAAGGCGGGCACACCAACTTTTTCGTGGGGTCTT
CCTCTTGTCACGCCGATGGTTGCTTCCACCTCGGCAGCACAACTCCATGAGCACTTTGAACCTCCGGCG
ATGCTGTGGGTTTCTTTCGGGCTCTTCTTTTAACTTTGGCGTCTGCACCAGCAGTTTTTACCCGAGTG
TATTCTACTATTTTCGGCCCCAAGGCGCAGGGCATCCCCTGATGGCAACACCAACATCATGGATTCCCT
TTGGGTATGGTGGGCCAATCCACTGCAGCAGCTCAGTCATCGGTGCGTCCCTTGGATCCAAGACAGCA
ATCACAATGGGCATTATTTACGGCATCATCATGGGAATTTTACGATTCCCTTGGAGCCATCGCTCAC
TTTGTGTTCTACAGAGCTGTTTCAAAGGGGCGACATACAGCCCCACATGGTGGGCCAGTACCTTCCCA
GTTGGCACTTTGAGTTTGGGTGCGCATTTTTTATCACAGAGCACCGGAGTGGAGTGGTTTAACTACTTC
AGCCTGTACTTGATTGCTTTAATGCTCTTTCATGTCATCGTGTCCACCATCGCCGGTACGATTGCAGTA
ATGAGAAGAATCGTCGGAAAGCTTAAATCTCAACTGGCC

RXS02590 - 3'-Region
TAAATTGCAGCGAGAGGTCTAAA

RXS02932 - 5'-Region
CACTACTGCGTTAAGGTATGAAAGTTCGCACACCAGCGATTTAATTCTGTGCCCACTAGCACGACC
ATTTCAAGTTTTAACTTTCTTGGAGTTTCTA

RXS02932 - coding Region
GTGTCCAAAACAGAAGAAGGCCGTTTCAGCGGCCATAATTATTTACGCGTTTCCAACCTTTCATTCTGCTG
GGCGCGATCATTTGCGTTTATCTTCCCAGAACCATTCATTCCGCTGACAACTACATTAATATCTTCCTC
ACGATCATCATGTTACCATGGGTTTGACCTTGACGGTGCCGATTTTCAGATGGTGCTTAAACGTCCA
CTGCCTATCTTGAAGGTGTAGTAGCGAGTTTGTGTCATCATGCCATTCCCTGGCGATCGTGGTTGCGAAA
ATGTTCAACCTTAACCCAGCACTCGCCGTTGGCCTTCTCATGCTGGGATCCGTTCCGGGTGGCACCTCC
TCCAATGTGATTGCGTTTCTCGCCCGAGGAGATGTCGCGCTATCGGTACCATGACCTCTGTGTCCACC

ATTGTTTCCCCAATCATGACGCCTTTTCCTCATGCTCATGCTGGCAGGTACTGAAACCGCCGTCGATGGT
GGAGGCATGGCGTGGACTTTTGGTACAAACAGTGCTGCTGCCGTGTGATCATCGGCCTAGTTCTGCGTGTC
TTCTTGAACAAGTGGATCGACAAGATTTTGCCGATCCTTCCTTATCTCTCCATCCTCGGTATCGGTGGC
GTGGTGTTCGGCGCAGTCGCAGCCAACGCGGAACGACTCGTGTCTGTGCGACTCATCGTGTTCGTTGCA
GTTATCGTGCACAACGTACTTGGATACGTTGTGGGATACCTCACC GGCCGTGTATTCAAATTTCCAGAA
GCAGCAAACCGCACCATGGCGATTGAAATCGGAACCCAATCCGCGAGGCCTCGCATCGGGAATGGCAGGA
CGATTCTTACCCCAAGAAGCAGCCCTTCCAGGTGCTGTGCTGCCCTTGGTCCACAACATCACC GGCGCA
GTTTATGTTGGGCTGGTACGAAACAGGCCTTTGACTAAGGCATCAAGGAAGAAGGAATCCGTCGCGGTT
TCCAGC

RXS02932 - 3'-Region
TAACTTATTTGCTGCCCGTTAGA

RXS03042 - 5'-Region
ATGACACCGGCGCGACGTATGGCATTACTGGCGTACCCCAATTTACGATGACATCTCTGCTCGCCTCGG
CGACGTCCTGGTTCCTTACGTTCTGATCGTT

RXS03042 - coding Region
TTGGTTC TAGCGTTCCCTCGTGCTGTTGCTCGTGTTCGGTCCATTGAGTCGCGGCTCTG
GGCTTTGGCTTGTCTAGTTCTGGCTACCTTTGGTGCTACCGTGGCGATCTTCCAAGAAGGTGCTTTGGC
ATCATCGACGATCCTCAGCCACTGCTGTCTTCTTGCCGATCATGCTCATCGGCCTGGTATTTGGTCTG
GCCATTGGATTACAGATCTTCTCGTTACTCGTATGCGTGAGGGCTTCACCAAGGGCAAGACTGCGGGC
AACGCAACGTCGAATGGTTTCAAGCACGGTGCCCGCGTGGTCACTGCTGCGGCGCTGATCATGGTGTCT
GTGTTTCGCGGCATTTCATAGCGCAGGACATGGCGTTTATTAAGACCATGGGCTTTGCTCTGGCCGTTGCT
GTGTTCTTCGATGCCCTTCGTTGTTTCGATGATGATTATCCCTGCAACAATGTTCTGCTTGATGACAAG
GCTTGGTGGCTACCTAAGTGGTTGGATAAGATTCTTCCCAACGTTGATGTTGAAGGTGAGGGTCTTAGT
GAACTACATGAGGCTCGCACCGAGGAAGTGAAGGAAAATGTAGGTGTCGGGGCT

RXS03042 - 3'-Region
TAGAGAAACAAAAAAGGCTGCTA

RXS03075 - 5'-Region
TGTGCAAAATTGCATTACAGGCTGAAAAATTCCTAAAGGGACTCCGTCCGAATAATTGGAAAGCCCAGAA
GAACAGTCAACTCCTAGATTAAAGGATAATC

RXS03075 - coding Region
GTGGCGAAATTCCTGTATAAGTTAGGCTCCACGGCCTATCAAAAGAAATGGCCGTTTCTTGCGGTCTGG
CTCGTGATTCTCATAGGTATCACGACGCTGGCGGGGCTGTATGCCAAGCCAACGTCGAGTAGCTTCTCT
ATCCCTGGTCTTGTATTCTGTACGACCATGGAGAAGATGCAGGAGCGTTTCCCTGGTTCCGATGATGCA
ACATCGGCTCCCACTGGTTCTGTCTGTCATTACAGGCACCGGAAGGCAAGACCCCTCACTGATCCTGAGGTT
GGGGCTGAAGTAAACCAGATGCTTGATGAGGTTCCGGGCGACTGGTGTGCTGAAGGATGCTGATTCCGTT
GTGGATCCTGTGTTGGCTGCGCAGGGTGTGGCTGCTCAGATGACCCAGCCCTGGAGGCTCAGGGTGTA
CCTGCGGAGAAGATCGCCGAGATATTGAGTCGATTAGTCCACTGAGTGCAGATGAGACTACCGGCATC
ATCTCGATGACTTTTGATGCAGATTCTGCCATGGATATATCCGCAGAGGATCGTGAGAAGGTACCAAT
ATTCTTGATGAATACGATGACGGCGATCTGACTGTTGTCTACAACGGCAACGTGTTTGGCGCAGCTGCA
ACCAGCTTGGACATGACCTCTGAGCTCATCGGCCTGCTGGTGGCTGCGGTGCTTCTTATCGTGACCTTC
GGTTCGTTTCATCGCTGCCGGTATGCCGCTGATCTCT

RXS03124 - coding Region
ATGACTCCTACCCTGGCGTCGATGATTGGTCTGGCTGTGCGTATCGACTACGCGCTATTTATCGTGTC
CGTTTCCGCAATGAGTTGATTCTCAGACTGGCGCTAATGATCTGGAGCCAAAGGAATTGGCTGAGCGT
CTGCGCACCATGCCGTTGGCTGCTCGTGCGCATGCGATGGGAATGGCTGTGGGCACTGCGGGTTCTGCG
GTTGTATTTCGCGGGTACCACGTTGCTGATCGCTCTGGTTGCTCTGTGATCATTAATATTCATTCTTA
ACCGTGATGGCCATTGCTGCCGCAATCACC GTTGCCATCGCAGTTCTGGTTGCTCTGTCTTCTCCCA
GCTCTGCTTGGCCTGCTTGGCACTCGCATCTTCGCAGCACGCGTGCCTGGACCTAAGGTTCCGGATCCT
GAGGACGAGAAGCCAACGATGGGTCTGAAGTGGTCCGCCTTGTGCGCAAGATGCCGGTGGCTTACCTG
CTGGTTGGCGCTCGTTTGGCTGCTGCAATCGCAATTCCTGCGACCAATATGCGCCTGGCCATGCCGACT
GATGGCACCTCCACGCTGGGCACCGCGCGCACGGGGTATGACATGACGGCAGATGCGTTCCGGCCCG
GGCCGCAACGCGCCCATGATTGCGCTTATCGACGCAACCGACGTCCCTGAGGAAGAACGCCCATTTGGTG
TTTGGACAGGCGGTGGAGCAATCTTGAACACTGATGGTGTGAAGAATGCTCAGATCACTCAGACCACG
GAGAATTTGATACCGCGCAGATCCTGTTACCCAGAAATTTGATGCGATCGATGAGCGCACCTCTGAGA

CTCTCGCAACTCTTCGTGCAGATGCTGAGACCTTCGCTGATGACACCGGCGCGACGTATGGCATTACTG
GCGTCACCCCAATTTACGATGACATCTCTGCTCGCCTCGGCGACGTCCTGGTTCCTTACGTTT

RXS03124 - 3'-Region
TGATCGTTTTGGTTCTAGCGTTC

RXS03125 - 5'-Region
TGACACCGGCGCGACGTATGGCATTACTGGCGTCACCCCAATTTACGATGACATCTCTGCTCGCCTCGG
CGACGTCCTGGTTCCTTACGTTCTGATCGTT

RXS03125 - coding Region
TTGGTTCTAGCGTTCCTCGTGTGCTGTTCCGGTCCATTTGGGTCCCATTTGATCGCGGCTCTG
GGCTTTGGCTTGTCAGTTCTGGCTACCTTTGGTGCTACCGTGCGGATCTTCCAAGAAGGTGCTTTCGGC
ATCATCGACGATCCTCAGCCACTGCTGTGCTTC

RXS03220 - coding Region
ATGGGCTTAAGGGAAATTTTGTCCAGCAAGTGGCTTGTGCGCATCCTCCTGGTAGGTATCGGATTGGGT
GTCGCACAGCAGCTGACCGGCATCAACTCCATCATGTACTACGGCCAGGTGTTCTCATTGAGGCTGGT
TTCTCCGAGAATGCAGCTCTGATCGCCAACGTGGCGCCAGGAGTGATCGCAGTTGTCGGTGCATTTCATC
GCACTGTGGATGATGGATGGTATCAACCGCCGTACCACCCCTCATTACCGGTTATTCTCTCACCACCATT
AGCCACGTATTGATCGGTATCGCATCCGTAGCATTCCCAGTCGGCGATCCTCTTCGCCCCCTACGTTATC
TTGACTCTGGTTGTGGTCTTCGTGGGATCCATGCAGACCTTCCTCAACGTAGCTACCTGGGTTATGCTC
TCTGAGCTCTTCCCCTGGCAATGCGCGGTTTCGCAATCGGTATCTCAGTGTTCTTCCTCTGGATCGCA
AACGCGTTCCTCGGATTGTTCTTCCCAACCATCATGGAAGCAGTAGGACTAACCAGAACCTTCTTCATG
TTCGCGGAATCGGTGTGGTTCCTTGATCTTCATCTACACCCAGGTTCTGAACTCGTGGACGTACC
TTGGAGGAGATTGATGAGGATGTTACTTCCGGTGTCATTTTCAACAAGGACATCCGAAAAGGAAAGGTG
CAC

RXS03220 - 3'-Region
TAAAAACCCAGACACTGCATAGATAACACG

RXS03221 - 5'-Region
CAAAAGTATTCAAAAAAGTTTGTATGTACGATTGACGGGACATATCGTGTCTGCCACGATTAAAGAC
ATTGGTGATGTGAATCACTGCCTACTACATC

RXS03221 - coding Region
GTGTTTCGTGACCCTGCACCTCCAAGTAAGGGCACGACAAACTTAGGAGACAAGATGGCTAGTACCTTC
ATTCAGGCCGACAGCCCTGAAAAAAGTAAGAAGCTGCCCCACTCACAGAAGGTCCGTATAGAAAGCGG
CTATTCTACGTTGCACTAGTTGCGACGTTTGGTGGGCTGCTCTTCGGATATGACACCGGAGTAATCAAC
GGTGCACCTCAACCCAATGACACGTGAGCTCGGACTAACCGCGTTTACCGAGGGTGTTGTAACCTTCTTCC
CTGCTGTTTGGTGCAGCAGCTGGTGCAGATGTTTTTCGGTTCGATTTCCGACAACCTGGGGTCGCCGAAA
ACAATCATCTCACTTGCAGTAGCTTTCTTTGTCGGCACCATGATCTGCGTGTTGCTCCATCTTTTGCA
GTAATGGTTGTGCGACGTGTGCTTCTTGGACTCGCAGTTGGTGGCGCTTCCACTGTTGTCCCTGTCTAC
CTGGCTGAACCTTGTCTCTTTTGAAATCCGTGGCTCACTGGCTGGCCGTAATGAGTTGATGATTGTTGTT
GGTCAGCTCGCAGCTTTTGTCAATGCGATTATTGGAAATGTTTTTGGACACCACGATGGTGTGTGG
CGCTACATGCTGGCAATTGCCGCAATCCAGCAATTGCCCTCTTCTTTGGAATG

APPENDIX B: AMINO ACID SEQUENCES

> RXA00001 (1-1128, translated) 376 residues
MATVTFK DAS LSYPGAKEPT VKKFNLEIAD GEFLVLVGPS GCGKSTTLRM LAGLENVTDG
AIFIGDKDVT HVAPRDRDIA MVFQNYALYP HMTVGENMGF ALKIAGKSQD EINKRVDEAA
ATLGLTEFLE RPKKALSGGQ RQRVAMGRAI VRNPQVFLMD EPLSNLDAKL RVQTRTQIAA
LQRKLGVTTV YVTHDQTEAL TMGDRIAVLK DGYLQQVGAP RELYDRPANV FVAGFIGSPA
MNLGTFESVKD GDATSGHARI KLSPETLAAM TPEDNGRITI GFRPEALEII PEGESTDLSI
PIKLD FVEEL GSDSFLYGKL VEGDGLGSSS EDVPESGQIV VRAAPNAAPA PGSVFHARIV
EGGQHNF SAS TGKRLP

> RXA00002 (1-684, translated) 228 residues
VLHREGKGGL LGAYIAGFEW GLEKDYHVLC EMDADGSHAP EQLHLLLEEI EKGADLVIGS
RYVPGGETVN WPANRELLSR LGNKYISVAL GAGINDMTAG YRAFRRELLE HLD FEELSNA
GYIFQVDVAF RAIKDGFDVR EVPITFTERE LGESKLDGSF VKDSLLEVTK WGVHRSEQI
SDFTSEVSKI ASRTVKDMEL GPKATTAKNA VPDFVSEVSN LAKGTFFK

> RXA00089 (1-999, translated) 333 residues
MATPASAPTS EPRLKRTRAK LFDWKLLIGI IFVAGLVVLS LLTGQYDIFG GDDGQLMFEA
VRIPRTVSLI LSGAAMAMCG LVMQLLTQNK FVEPSTTGTT EWAGLGLLFV IYFVPAATVL
DRMLGAVVFS FIGTMVFFLF LRRVTLRSSL IVPIIGIMLG AVVSSISSFF ALQFDMLOQL
GTWFAGSFNT VFRGQYEV LW IVVIVVIAVF FFADRLTVAG LGEEIATNVG LNYNRMVLIG
TGLIAIATGV VTVVVGSLPF LGLIVPNVVS MFRGDDLRSN LPWVCLTGIA IVTICDLISR
TIIAPFEIPV SVILGIIGAV VFVIMIVRQR GRG

> RXA00090 (1-1119, translated) 373 residues
VAVDKDIENR TSDLSRWETM EESATVEGRT DVELASAPSK RRTSGAFQTA RAKRRYWIIM
AALLVTALAF TWGLIWKYKNP MPVGHPAFAL IAERRMESVF VMLIVAVCQG FATVAFQTVT
NNRIITPSIM GFESLYTLIH TSTVFFFGAT ALLATRNL EM FVGQLVIMVL LTLVLYTWLL
SGKRGMHAM LLVGIIIGGG LGSISTFMQR ILTPSEFDIL SARLEGSVNN AETEFPIAV
PLVVVASVLL LLSSRRNLNV GLGKDAATNL GINHRRSSIY TLVLVSVLMA VSTALVGPM T
FLGLVATLA YQFADTYDHR YILPMSALIG FVVL SGAYFV MNHVFRAQGV VSIIEMVGG
TVFLIVILRK GRL

> RXA00099 (1-1173, translated) 391 residues
VKNPRLIALA AIILTSFNLR TAITALAPLV SEIRDDLGV S ASLIGVLGMI PTAMFADAA F
ALPSLKRKFT TSQLLMFAML LTAAGQIIRV AGPASLLMVG TVFAMFAIGV TNVLLPIAVR
EYFPRHVGGM STTYLVSFQI VQALAPT LAV PISQWATHVG LTGWRVSLGS WALLGLVAAI
SWIPLLSLQG ARVVAAPSKV SLPVWKSSVG VGLGLMFGFT SFATYILMGF MPQMV GDPQL
GAVLLGWWSI LGLPLNILGP WLVTFTNC F PMVVIASVMF LIGNGGFCLA PDVAPWLWAT
LSGLGPLAFP MALT LINIRA ETSAGASALS SFGQGLGYTI ACFGPLL TGF IVDATGSFRT
IFLLFAGATL FVIRGGYFAT RQVYVEKLLN R

> RXA00123 (1-1119, translated) 373 residues
MPKNYDINGA IRRRDMLRRR YLPDSANSTP VP EEVSPLTR YVTDGIPKRP PLGATVADGL
KFAEGASNRM VMSLYPAPSK PAIEELAEAW DLHPTIVEDL LLGQQRPKLD RYEDIIFIAI
RSARYIDSRE EVDFSEFHIL MKPQAI AILC QDNQWIDGTS AASFNSPEEI DKRIKTL LAD
AELLSSGPRA AAYRL LDAIV DGFSPVLRGI AIDQEQIERQ VFSGDAVAE RIYNLSQEII
DMQHTTSSVT EVVQRLNKDF IRSGMSEELR AYLDDVADHL TRDNTRVSEY RESLSQILNV
NATLVAQRQN EDMKKISGWA AIIFAPTLVS SIYGMNFDIM PELHWA FGYP LALLAMLGFT
LLLYWIFKRS KWM

> RXA00160 (1-573, translated) 191 residues
MLNIARNRNM KRRLAIAAFV ATATATATMA PASAQTDYAG LSSGVADTVA EAAGVATTAV
APAATVARPA NGTFTSGFGP RWGTFHNGID IANSIGTPIY AVMAGTVISS GPASGYGQWI
RIQHDDGSIS IYGHMEYLYV SVGERVAAGQ EIAGMGSQGF STGSHLHFEI HPDGVTPVDP
QAWLANHGIY V

> RXA00193 (1-843, translated) 281 residues
MQATLKKYFP VFVLP TLLAF MIAFLVPPFIV GFFLSFTKFT TITNAKWVG I DNYVKAFSQR
EGFISAFGFT VLVVIVSVIT VNIFAFLLAW LLTRKLRGTN FFRTVFFMPN LIGGIVLGYT

WQTMINAVLS HYATTISADW KFGYAGLIML LNWQLIGYMM IIYIAGLQNV PPELIEAAEL
 DGVNKEWMLR HVTIPMVMPS ITICLFLTLS NSFKLFDQNL ALTNGAPGGQ TEMVALNIIN
 TLFNRMNVEG VGQAKAVIFV VVVVVIAYFQ LRATRSKEIE A

> RXA00203 (1-912, translated) 304 residues
 MLNNGALVGL IALCVGLFIA TPHFLTIPNL INIGIQSATV AILAFGMTEFV IVTAGIDLSV
 GSVAALGAMT SAYFFAEVGL PGWITLLIGL FIGLLAGAIS GISIAYGKLP AFIATLAMMS
 IARGITLVIS QGSPIPSAPA VNALGRTYFG IPMPILMMAL AGIVCWFILS RTVLGRSMYA
 IGGNMEAARL SGLPVKKILV MVYALAGVYA ALAGLVMTGR LSSAQPPQAGV GYELDAIAAV
 VIGGASLAGG TGKATGTLLG AILLAVIRNG LNILNVSSFV QQIVIGCVIA LAVGFDVIRN
 KTSK

> RXA00204 (1-1572, translated) 524 residues
 MVNSEQALHQ HDPAPILQLD KVSKEFGPVN VINQVSDVDR PGRVLALLGE NGAGKSTLIK
 MMSGVYQPDG GQILVDGKPT TLPDTKTAE FGIATIHQEL NLVPTMTVAE NVMLGRTPRK
 WGLVNFKHLR RQAQAALDLI GVDVDLNAQV GSLGIARQQM VEIAKALSMN ARILILDEPT
 AALTGREIDQ LFKVVDQLKE KGVAMVFISH HLDEIARIGD TVSVLRDQGF IAELPADTDE
 DELVRLMVGR SIENQYPRSA PEIGQPLLEV KNLNAEGRFT DISLTVRAGE VVGLAGLVGA
 GRTEVVRSIA GVDKVDSEV IVAGKKLRGG DISEAIKNGI GHIPEDRKAQ GLVLGSSVED
 NLGLATLAST ARAGLVDRSG QHKRAAEVAE KLRIRMASLK QPISDLSGGN QQKAVFGRWV
 LAGSNVLLLD EPTRGVDVGA KVEIYNIINE MTEKGGAVLM VSSELPEVLG MADRILVMSG
 GRIAGELPAK GTTQDDVMAL AVSQVDDISIT EEAEEIENT KEDR

> RXA00270 (1-888, translated) 296 residues
 MIGAFEFGLL YGVVALGVYL TFRVLNFPDL TVDGSLLTGA ATAATALMSG WPPLMATAAG
 FVTGFIAGMI TGLLHTKGKI DGLLAGILTM IALWSVNLRI MGGANVPLLR TDNLFTPLRD
 AGLLGTWAGP AILAVAVGIL GLIVIWFLNT DIGLSLRSTG DNGPMVQSFG VSTDFTKILT
 ISLSNGFVGL AGALIAQYQG FADISMGIGL IVIGLASVIL GQAIFFGQRRV WLAVLAVIVG
 AIAAYRLIIFA ALRVGLDPND MKAISAILVV VAMLLPRWRA KFSKAPKPKQ PVAVEA

> RXA00311 (1-855, translated) 285 residues
 MEHSPEGKRG FFTSSVMAGC SVGNVLAGLV FIPFLMLPEE HLMSWGWRVP FLISALVIVV
 AYFVTRILEE ASTEKAEDA GAPALAVLRT QGIDVARVEL ITFFAVVQTT FNVYALAYAA
 NEIGIDRSFM VMVNTIALGL SIGTIPLAAW VSDRIGRKPV LLFGAITCAI TTYFYFQAIS
 EADLVLFAL CLVNQGLFYS CWNGVWTIFF PEMFASSVRY TGMAMGNQLG LIIVGFAPTI
 ATALYAWNGW EAVAGFIIGA IALSAAVILT TKETAFTKLE DLGKK

> RXA00312 (1-426, translated) 142 residues
 METVRTATAA PETASLKLRE AESPAKSPKK AALASLLGST LEYYDFVIYG TASALLFNHL
 FFPQGDVVA TIGSLASFGV AYIARPIGGL VMGHVGDKIS RKTALMVTLM IMGIASISIG
 LLPTYGQIGI WATVLLMIAR IA

> RXA00345 (1-951, translated) 317 residues
 MAGMKKLLWT LPILPLVLG CSTGSADSAD STNAAGSNSL KVVSTSTQVWA DVAEAVAPDV
 DIEAIIITGGD IDPHSFEPSE TDMKVSEAD IIVGGGGYD SWLYGTLEDD DRIIHALDLS
 EHDHSEHDDH EHEAEEAHEH DHDEEGHDHD VDNEHVWYST EYVSEVAEEF AEKVTELDPE
 AQADATAVTT KMDELHNQIH DLPVRIAQT EPIADHILSH SDMVESTPEG YRATTLESE
 PTAADVASFQ DAINNGDLV LIYNPQSAST VATSLKDLAE EKGIPVVEIY ETPQNTENFL
 DAFTKAVDDL TAATNQV

> RXA00378 (1-1773, translated) 591 residues
 KSWRSYPSWF AFDHGTLTQN EIYFDVACGI TVLLLAGRLL TRRRSQSSLL AELGRLQIDP
 QRIVTVVRKH RLKRVVQELN IPVQEVVRND DVKVPNTTI PVDGTVIGGG SRIAASIIMG
 QDQRDVKVND KVFAGSLNLE SEIKVRVIRT GHRTRIAAVH RWVKEATLKE NRHNRAAIRS
 AGNLVPITFT LAVVDFCLWA LISGNINAAF TTTLAVLACV APVALALSAP LATRNSIEAA
 ARHGILVRSG EIFRVLDDVD TAVFNRVGTI TDGEMTVETV TADKGEDPEL VLRVAGALAM
 ESHHAISKAL VKASREARDT GAGGEDVPHW IEVGNVEITE AGSFQATIEL PLIKPSGEKI
 MRTTEALLWR PRSMTEVREH LSPRLVAAAT SGGAPLIVRW KGKDRGVITL SDHVRSDSSD
 AIIAIEEQGI ETMMLSRDTH PVARRYADSL GITHVLGIA PGKKAQVVRA VHTRGSTVAM
 IGDESVMDCI KQADVGVLMG VDRPSDLRDD SDDPAADVIV MREEVMSVPT LFKLARRYAK
 LVNGNIALAW IYNGVAMVLA VSGLLHPMAA TVAMLASSLL IEWRSGRARK Y

> RXA00412 (1-1080, translated) 360 residues
 VSHTASTPTP EEYSAQQPST QGTRVEFRGI TKVFSNNKSA KTTALDNTVL TVEPGEVIGI
 IGYSGAGKST LVRLINGLDS PTSGSLLNG TDIVGMPESE LRKLRNIGM IFQQFNLFQS
 RTAAGNVEYP LEVAKMDKAA RKARVQEMLE FVGLGDKGKN YPEQLSGGQK QRVGIARALA
 TNPTLLLADE ATSALDPETT HEVLELLRKV NRELGITIVV ITHEMEVVRV IADKVAVMES
 GKVVVEYGSVY EVFSNPQTQV AQKFVATALR NTPDQVESED LLSHEGRLFT IDLTETSGFF
 AATARAEEQG AFVNIVHGGV TTLQRQSFGK MTVRLTGNTA AIEEFYQTLT KTTTIKEITR

> RXA00413 (1-897, translated) 299 residues
 MKLRRITTTA IAGLFAATAL VACGSDSDGS STTVAEGTEG VTIRIGTTDA AKEAWTVFED
 KAAEEGITLD IVPFSDYSTP NEALAQDQLD VNLFOHLKFL AEYNVGSAGAD LTPVGSSEIV
 PLALFWKDHG SIDGIDGESV AIPNDPSNQG RAINVLVQAG LVTLKTPGLV TPAPVDIDEA
 ASKVSVIPVD AAQAPTAYQE GRPAIINNSF LDRAGIDPNL AVFEDDPESE EAEPYINVFV
 TKAEDKDDAN IARLVELWHD PEVLAAVDRD SEGTSVPVDR PGADLQEILD RLEADQENA

> RXA00431 (1-675, translated) 225 residues
 MVSIDTYNAC VDFPIFDAKS RSMKKAFLGA AGGAIGRNQD NVVVVEALKN VNLHLREGDR
 VGLVGHNGAG KSTLLRLLSG IYEPTRGSAD IRGRVAPVFD LGVGMPEIS GYENIIIRGL
 FLGQTRKQMK AKMEEIADFT ELGEYLSMPL RTYSTGMRIR LALGVVTSIE PEILLLDEGI
 GAVDAAFMAK ARDRLQALVE RSGILVFAST QRLSCQLCNT ALWVD

> RXA00444 (1-777, translated) 259 residues
 LLIPATLAML LIIGPIFALL LQIPWDRSWE LLTAPESLGT ARLSIGTALF STALCAIVGF
 PLALALHLYE RSHPRVTSVL TVLVYAPLVL SPVVSGLALT FLWGRRGFLG SWLDQVGLPI
 AFTTTAVVEA QVFVALPFFI STVTTALRGI PKQFEEIAAT EGATRWEIMH KMI I PLAMPG
 IFTGMILGFA RALGEYGATL TFAGNIAGVT RTIPLHIELG LSSNDMDKAL GAVIMLLAVY
 VLIIGAIGAL RLFSKVRKV

> RXA00445 (1-912, translated) 304 residues
 MADLSIEHVS RFFGDAIALN DVSLTVPSGS ITAIIGPSGS GKTLLRLLA GLDSPDEGTV
 SIGNKIAKLG DTALCFQDSP LYPHLNVWEN VAFPLKLKAT NTADDEVVKKR VSDVLEMLEI
 APLARRKITE LSGGQKQRVG IARALVRDVE VYLFDEPMAH LDQALARDIV ADLRKIQQSL
 GLTFVYVTHS KSEAFALADQ IVVLVDGQVA QVGEAEELVE KPKTLEIAEF LSPTELVRR
 RGDAVEAWRP EDTQLARGGT ATVEAVTYLG REWLVTQTEG HAVSEEKFDV GESVTLTQKK
 VFSF

> RXA00466 (1-987, translated) 329 residues
 VQSRLSKILR SSVVGVAULA LLAGCSNNAD DTDADSTSTG NSAFPVSIEH EFGTTTIDDV
 PERVVTLGVT DADIVLALGT VPGNTGYKF FENGLGPWTD ELVEGKELTL LDSDSTPDLE
 QVAALEPDLI IGVSAGFDDV VYEQLSDIAP VVARPAGTAA YAVAREEATN LVARAMGQSE
 KGQELNEETD ALIQAARDEN PSFDGKTGTV ILPYQGYGA YLPGDARGQF LDSLGISLPE
 AVLSRDTGDS FFVDVPAESV KDVDGDVLLV LSNDENLDIT AENPLFETLN VVQKDAVIVA
 TTEERGAITY NSVLSVPFAL EHLAPRIAE

> RXA00482 (1-648, translated) 216 residues
 MRISSKLVTT ALLAAISLFG ISTAQADIF DGRLAGGSS QVSNLSSVPE NLALPEIENS
 IDLERYKGKW YQVAAIPQPF SLQCSHDVTA DYGVIDSITI SVTNKCGTFF GPSVIEGSAK
 VVSNASLKVS FPGIPFQSED NQANYRVTYI EDDYSLAIVG SPSRSSGFIL SRTPQLSSDQ
 WSHVRNITED SGWWPCAFIT VPATGGLNTA TPLCTL

> RXA00523 (1-750, translated) 250 residues
 VLRNQLASPD IIGISSGASA AGVICIVFFG MSQSAVSAIS LCASLAVALL IYLVAYRGGF
 SATRLILTGI GIAAMLNSLV SYLSKADSW DLPTATRWLT GSLNGATWDR AMPLIVTTVV
 LIPLLVANAR NVDLMRLGND SAVGLGVATN RTRVIAIIAA VALIAVATAA CGPIAFVAFV
 SGPIAARILG SGGSLIIPSA LIGGLIVLIA DLIGQYFLGT RYPVGVVTGA FGAPFLIYLL
 IRSNRAGVTL

> RXA00525 (1-660, translated) 220 residues
 MSLAESILLA LTSLSRNKMR ALLTLLGVII GIASVIGILT IGKALQDQTL NSLES LGAND
 LSAQVEERPD EDSPEPDMFA FSGAANSSGN LIPEETVDTL RDRFAGSITG ISVGGMGTOG

TLIGDTADLK SDLLGVNEDY MWMNGVEMNY GRAITQDDVA AQRPVAVIAP DTFNTLFDAN
PNLALGSEVA FELNGQETFL RVIGVYKEAA AGGLVGSNPT

> RXA00556 (1-594, translated) 198 residues
YTPYTVANDI THTKDGLNTL SIRAAQGVDQ DSLKGSQTY FDALYANNDS HHVAMLDLFRK
QIEEFNTILG AMSLGISAIG GISLLVGGIG VMNIMLVSVT ERTREIGVRK ALGARRRDIR
LQFVVEAMII CFIGGILGVL LGGILGLIMS SAIGYISLPP LSGIVIALVF SMAIGLFFGY
YPANKAAKLD PIDALRYE

> RXA00596 (1-453, translated) 151 residues
MLNALKFIPW LIGQIFLSGF SVITAAVKKD TGFNPVVIRY PLRVTTDFQI AALSTCITAT
PSTLSLGLRE PRKPGDPTIL LIQAVFGSDP VEVFESIADM EQRLVPSVAS IDHGVPGQGP
YKEIRPSDAE WPSREIADTA QNTVSQDKRE F

> RXA00634 (1-1383, translated) 461 residues
MWERFSFYGM QALLVYYLYF DVAAGGLGLD QTQATGLVGV YGALLYLCCW AGGWVSDRVL
GAECTLLGGA ISVTIGHLVL AGLGKGIGLA IGLGCIAGS GFVKTAATV LGSRHGEQEG
DAKADPAFQL FYLGINVGAL LGPLLTGWLS SRYSEFMGFG AAVALMIGGL GIYAALRKPM
LQSFPLEVKK ALLRAQNPAE KHVISTAFAA VAVLCGVLLY LLLTETVSAD QLAGALLLV
IGAALWLIIQ PLRHPQVSSE EKRKVLAFIP IFVCSTAFWA VQAQTYGVLA VYSQERVDRM
VGDFEIPAAW SOSLNPFIL ALSIPISLWF MRGSRAPRVK IGISIGVIA GSGLLVLIPIF
VGMPLAPVWV LPLSVFLISL GELFIGPGGM AATAHHAPRI FATRESALYF LTLAIGMSIA
GNVSKFYDPT NHTSELRIFA VFGISIIVIG VGSLMVAKKV G

> RXA00665 (1-438, translated) 146 residues
MSSSTLLLAS GQVTLAADY TLSHTPSDGI LVVLGAFAMIL TFMTLIMLGR LTPMVAMLLV
PTIFGLIAGA GLGLGDMALD AIKDMAPTAA LLMFAIMFFG IMIDVGLFDP LIRVITRVLH
DDPAKVIGT AVLAGVVS LD GDGSTT

> RXA00702 (1-1320, translated) 440 residues
LGLPPAVMRK RVEETLDBLG IAELEYPVLA ELSGGEQQRV AIGAVLTTRP ALIILDEPTS
ALDPNGAEDV LATVTKLAHD LAMTVVLAEH RIERVLQYVD RVAHVGADGH VTVGTPEEIM
ADSDVAPPIV ELGRWAGWAP LPLSIRDARA HSADMRKRLY QRGVLVKNLH NHAVQPLLIA
EDIMVDFPEI RAVDGVNLNL NSGEITVLMG RNCCKGSSLL WALQSGGTRN QGSVQVLDEA
AGFSWTDPKT LKPAKRRNLV SMVPQTPTDI LYESTVHAEL ARSDKDAAAP AGTTREILDS
LVPNIPDHLH PRDLSEGQKL SLALSIQLAA KPRVVFDEP TRGLDYDGKK SLARSFQQLA
DDGHAILVVT HDVEFSALCA DRVLFMASGK IISDGTAVEI LPASPAYAPQ VAKITAGIQE
ESHWLTVSAV KAALGHGEIS

> RXA00728 (1-792, translated) 264 residues
VAAAIIVALL AWFIIISALNN EAYGWDITYRS YLFDTRIATA ALHTIALTLL SMILGVVLGA
ILAVMRMSGN PVMQGVAWLY LWIFRGTPYI VQLVFWGLLG SLYQSINLGF AEIDLQSLLS
NMFLLAIVIGL GLNEAAYMAE IVRSGIQAVP EGQMEASKAL GMNWSMTMRR TILPQAMRII
IPPTGNELIS MLKTTSLVVA IPYSLELYGR SMDIAYSLFE PVPMLLVAAS WYLVITSILM
VGQYYLEKHF EKGSTRTLTA RQLA

> RXA00732 (1-822, translated) 274 residues
MLVQMTSTLM ISAPMLAIGG IIMAVRQDLG LSWMVVSIP VLIIVVALII VRMVPLFQTM
QKRIDRINQI IREQLTGIRV IRAFVREDVE RERFTTASKD VADIGVRTGN LMALMFPAVM
LIMNLSAVAV IWFGAFQVES GETQIGTLFA FLQYIMQILM GVMMAAFMFV MVPRAAVSAD
RIGEVLETP SVQAPETPAQ PSTSAGEIVF NNATFAYPGA DDPVLNNVSF RVAPGSTTAI
IGSTGSGKTT LIGLVPRLFD VTEGDVTVDG TDVR

> RXA00734 (1-453, translated) 151 residues
RHLRYGNEDA TETQLWQALA IAQAADFVRE MPEGLDSEIA QGGTNVSGGQ RQRLAIARAL
LKQPEIYIFD DSFSALDVST DAALRRALST NLPDATKLIV AQRVSTIRDA DQIVVLNNGE
VVGIGTHTNL LNTCGTYREI VESQETAQAQ S

> RXA00759 (1-924, translated) 308 residues
MLRYVGRLL QMIPVFFGAT LLIYALVFLM PGDPVQALGG DRGLTEAAAE KIRQEYNLDK
PFIVQYLLYI KGIFVLDFGT TFSGQPVIV MARAFPVTIK LAIMALLFES ILGIIFGVIA

GIRRGGIFDS TVLVLSLIVI AVPTFVIGFV LQFLXGVKWG LLPVTVGSNT SITALIMPAV
VLGAVSFAYV LRLTRQSVSE NLRADYVRTA RAKGMSGFNV MNRHVLRLNSL IPVATFLGAD
LGALMGGAIV TEGIFGINGV GGTLYQAILK GEPTTVVSIV TVLVIVYIIA NLLVDLIYAV
LDPRIRYA

> RXA00760 (1-1032, translated) 344 residues
MPNNEFHTNH SLGQDDQTPD QAHFFPQGRG EALVRPGQEH FIAATDETGL GAVDAVADDS
APTSMWGEAW RDLRRRPLFW VSAVLIILAL LLAAVPQLFT STDPQFCVLA NSLDGPQSGH
PFGFDRQCD IFARTVYGAR ASVAVGVLTT LLVALIGTVF GALAGEFGGI MDTILSRITD
MFFAIPVLVA AIVVMQMFKE HRTIVTVVLV LGLFGWTNIA RITRGAVMTA KNEEYVTSAR
ALGASKAKIL LSHIMPNAAL PIIVYATVAL GTFIVAEATL SFLGIGLPPS IVSWGADIAG
AQTSLRTQPM VLFYPAMALA LTVLSFIMMG DVVRDALDPK SRKR

> RXA00761 (1-591, translated) 197 residues
MTTNIPQTPN HEGEQPLLEL KDLKISFTSS TGVVDAVRGA NLTIYPGQSV AIVGESGSGK
STTAMSIIGL LPGTGKVTEG SIMFDGQDIT GLSNKQMEKY RGSEIGLVPQ DPMTNLNPFVW
RIGTQVKESL RANHVVPGESE MDKRVAEVL EAGLPDAERR AKQYPHEFSG GMRHRALIAI
GLAARPKLLI ADEPTSA

> RXA00774 (1-654, translated) 218 residues
MDKATDALLR TSLASAESAL GNAEKLEELR TGCESQAVEL LALETFVARD LRQVVSIIYI
VEEITRMGAL AMHVANSVRR RYPDPVIPED MRGYFKEMAR LAADMTDHIR QILIDPEPDL
ALEMAKSDDA VDDLHQHIMR ILTLRPWPHD TKSVDLTLT SRFYERYADH TVNVAARIYI
LSTGLHPEEY MEKREQQRAD ADMEKRWAELE ERQFRTSE

> RXA00775 (1-771, translated) 257 residues
MSKLKLNVDN IYYGDFHAVQ NVNLEVPARS VTAFIGPSGC GKSTVLRISIN RMHEVTPGAY
VKGEILLDGE NIYGSKIDPV AVRNTIGMV F QKANPFPTMS IEDNVVAGLK LSGEKNKKKL
KEVAEKSLRG ANLWEEVKDR LDKPGGGLSG GQQQRLCIAR AIAVEPEILL MDEPCSLDP
ISTLAVEDLI HELKEEFTIV IVTHNMQQAA RVSDQTAFFS LEATGRPGRL VEIGPTKKIF
ENPDQKETED YISGRFG

> RXA00776 (1-921, translated) 307 residues
MTNNVVTPRM DEPLKKSSAF TDISSSRKTT NTAATVIIYG AMLIAAVPLV WVLWTVISRG
IAPILTADWW STSQAGVMLM LPGGGAHAM IGTFMQAVVT SVISIPIGIF TAIYLVEYSN
GNRLGRLTTF MVDILTGVPS IVAALFVYSL WIVLFGFDRS GFAVSLSLVI LMVPVIIRNT
EEMLRVVPQD LREASYALGV PKWKTIKIV LPTALSGIVT GVMLAVARVM GESAPVLVLV
GSSQAINWNP FGGPQASLPL MMLDMYKAGT APATLDKLGW AALTIVLIIA VLNIGARIIS
AKFSVKQ

> RXA00777 (1-1065, translated) 355 residues
MATNESVSEK QRLDTRVQA HPVAVNANSS QTKPSKKIVA EGGGSVKRPG DRIFEVLSTA
SAAIITAIII AIAAFLIWRV VPALMRNAEG IGGFFTYSGA WNTTDIDAMY FGIPNLLAAT
LLISVIALII AMPIALGIAI FLSNYSKRL VKPLGYMVDL LAAVPSIVYG LWGWQVLGPA
LSGFYTWIES WGSFFLFFAT YQNSPSFATG RNMLTGIVL AVMLPVLIEA TAREVFIQTP
KGHIESALAL GATRWEVVRL TVLPFGMSGY VSGAMLGLGR ALGETMALYM VVSPSSAFRF
SLFDGGTTFA TAIANAAPF NDNTRAGAYI SAGLVLFALT FIVNAGARAM VNRGK

> RXA00828 (1-369, translated) 123 residues
EHQFVARTVR DELEIGPKIM KVDASERIEE LLDRLRLRHL ENANPFTLSG GEKRRLSVAT
ALVAAPKLLI LDEPTFGQDP ETFTLVTML RELTDNGISI VSVTHDPDFI AALGDHHIEV
SAK

> RXA00832 (1-555, translated) 185 residues
TLTAVVYGGF LFRQMGAAQAG EFQEVEVAEK ADDAAKWEVP FRGLILIIITV LPIVLLSHDM
ATVMDEVLAS LGAPVAMAGL IIATIVFLPE TITSLKAAWT GEIQRVSNLA HGAQVSTVGL
TIPAVLVIGV ITGQDVVLGE TPINLLLLGT TIAVTAIAFS SKKVS AVHGS VLLMLFGVYM
MSMFA

> RXA00934 (1-789, translated) 263 residues
PSFSMAALPF AEGPIVATYH ASSSGSKLLK AFLPVLSPML EKVRAGIAVS EMARRWQVEQ

VGGDPVLIPN GVETSMFKAA RQIEPNPVE IVFLGRIDES RKGLDILLRA LTRLDRPFTC
TVIGGGTPRE VAGINFVGRV SDEEKAAILG RADIYVAPNT GGESFGIVLV EAMAAGCAVV
ASDLEAFSLV TDSEAAQPAG VLFKTGSDAD LAKKLQALID DPSSRSTLIA AGLKRANAYD
WSTVSTQVMA VYETIAIDKV RLG

> RXA00939 (1-168, translated) 56 residues
GVLLGGVTMS IGMVLVHEASV LLVIAIAMLL LRPTLKEDKD KADVSTADAA KETLSA

> RXA00942 (1-204, translated) 68 residues
LSTKNYHVEG LTCANGVASV EDEIGIVAGT QGVDIDIETG RVTVTGEGFT DEEIIIEAVAN
AGYKVSGR

> RXA00950 (1-906, translated) 302 residues
MNTPAVQVQN LSLSFGSFTA VNGLSLTVEQ GSIHGFLGPN GAGKSTTIRA LIGVLKPQTG
SVAILGQDPV AHPDVLRRVG YVPGDATLWD NLTGAEVFRA LESLRKTPSN RALENELIDA
FQLDPSKKIR EYSTGNRRKV SLIAALSHEP ELLIVDEPTA GLDPIMEQVF VTYVRKARTN
GASVLLSSHI LSEVEQLCDY VTVLKEGRAV ASNEVSYLRK ISAHRITATI PAVPQHLAGR
GEVDFDAGHL SITCDASEVP DILRIIIDAG QQDIISTAAS LEEIFLRHYG ETVSGSESKA
SQ

> RXA00960 (1-459, translated) 153 residues
LKNDVDVNVA GFVVPLCATI HLAGSMMKIG LFTFAVVMY DMEVGVGLSI GFLMLGITM
IAAPGVPGGA IMAATGMLAS MLGFNTEQVA LMIAAYIAID SFGTAANVTG DGAIIVIVNK
FAKGQLHTTS PDEIEEDDRV AFDITPSDVE HHK

> RXA00980 (1-639, translated) 213 residues
MFVGVNGHAI GIVAVADAVR SDSASAIESL HKAGIQVMA TGDHRVAQN VASKLGVDEV
YSELLPEQKL ELVRDLQAAG KTVAMVGDV NDTPALAAAD IGVAMGVAGS PAAIETADIA
LMADRLPRLA HAVTLAKRTV RTMRINILIA LATVMVLLAG VLFGGVTMSV GMLVHEASVL
LVISIAMLLL RPTLKEDAAQ ASDIKRSEIQ QIA

> RXA01000 (1-540, translated) 180 residues
MLAARGVGPY WLRTVLRVFV AVIRAFPEVV IAIILLTVTG LTPFTGALAL GISGIGQQAQ
WTYEAIESTP TGPSEAVRAA GGTTPEVLRW ALWPQVAPSI ASFALYRFEI NIRTSAVLGI
VGAGGIGSML ANYTNYRQWD TVGMILLIVV VATMIVDLIS GTIRRRIMKG ASDRVVAPSN

> RXA01002 (1-417, translated) 139 residues
PTEHDKQIAF HALESVGILD KVVTRAGALS GGQKQVAIA RALSQDPSVM LADEPVASLD
PPTAHSMVRD LENINNVEGL TVLVNLHLID LARQYTTRLV GLRAGKLVDYD GPISATDKD
FEAIYGRPIQ AKDLLGDRA

> RXA01003 (1-804, translated) 268 residues
MTTPSSTLIP QKPRAGVKTY LIIGAIVVFT VATATPALGG IELDFASIAA NWRNGANKLL
QMLQPNFAFL PRTWLPMLET LQMALVGAVL SAAVSVPLTL WAAQATNTSA IGRGIVRTII
NVVRSVPDLV YATILVAMVG VGALPGILT FLFNLGIVVK LVSEAIIDSTE HPYMEAGRAA
GGSQFQINRV SALPEVMPLF ANQWLYTLEL NVRISAILGI VGAGGIGRLL DERRAFYAYA
DVSVIILEIL IVVIVIEVIS NALRKRLV

> RXA01006 (1-858, translated) 286 residues
MTTSQILRRI GQAVLVLLVT FTLAFIMLSA LPGDAVSARY SSPDLGLSPE QIAQIRESYG
ADESLIAQYF STLGGFLVGN FGYSVQTGTA VATQLAEALP GTLTLAILAF LLAAILALVI
SILATMDRFA WIKGIFQALP PFFVSLPSFW LGIILIQIVS FRLGWVPVIG TTPAQGLILP
TITLSIPITA PLAQVLIRSI EEVKAQPFIA AVRARGAGEM WIFFRNIIRN ALLPTLTIAI
ILFGELVGGA VVTEAVFGRA GLGQMTVNAV ANRDMPVMLA IVVIAA

> RXA01012 (1-1641, translated) 547 residues
MTTPLLEIND LVVSYQTAKG LVHAVNNVSL EVHPGQITAI VGESGSGKST TAQAVIGLLA
DNAEVDSGRI SFNGRSLVGL NAREWKNVRG TKIGLIPQDP NNSLNPVKTI GASVGEGLAI
HKRGTAERK KKVIELLERV GIDNPEVRYD QYPHELSSGM KQRALIAAAI ALEPELIAD
EPTSALDVTV QKIILDLED MQRELGMGIL FITHDLAVAG DRADRIVVMQ KGEVRESGYA
ASVLTDPQHE YSKLLADAP SLTIGEIPTR VPAVDPEVAQ AKGPLLVVDK FRKEHQKGKE

GAFVAANDIS FEVLPGTTHA IVGESGSGKT TLGRAIAMFN TPTSGSISVS GKDITNLSKA
 QQRELRLQIQ LVYQNPYSSL DPRQTIGSTI AEPLRNFTKV SKQEADEKVA HYLELVALDP
 ALATRRPREL SGGQRQRVAI ARAMILEPEL VVFDEAVSAL DVTVQAQILR LLDDLQRELQ
 LTYVFISHDL AVVREISDTV SVMSRGNQVE LGKTAEVFNN PQTDFTRRLI DAIPGSRYRG
 GELNLGL

> RXA01013 (1-795, translated) 265 residues
 LGNPWTRPAA VISIVVLAVA VLMALVPGLF TSQDPFTGDD VALLGPSGTH WFGTDSVGRD
 LYSRVYGAR ETLLGALIAV LVGLIVGTLI GLLAGAQRGW VDTVLMRFVD VLLSIPALLL
 SLTVIILLGF GTMNAAIAVG ITS VATFARL ARSQVMTVAG SDFVEAAYGS GGTQAQVLF
 HILPNSLTPV FALAALQFGS AILQLSVLGF LGYGAPAPTP EWGLLISDAR DYMATSWWLT
 VLPGFVIIAV VMSANYLSRI IQKEA

> RXA01070 (1-1386, translated) 462 residues
 MANATAQKGR FGLPGWMTGF GAQVIAGLIL GLILGLVARG MDSGAADGEA SWLTGLLSGV
 GSAYVSLKLV MVPPLVFAAV VTSVAKLREV ANAARLAVST LVWFAITAFF SVLGLIAVAL
 IMQPGVGSTV DASNAADPSR VGSWLGFQIS VIPSNILGLS GSYSENSGVN LSFNVLQILV
 ISIAIGVAAL KAGKSAEPFL KFTESFLKII QIVLWWIIRL APIGSAALIG NAVATYGWSA
 LGSGLKFLVA IYVGLAIVMF VIYPVVLKLN GIPVLGFFKR VWPVTSLGTV TRSSMGVMPV
 TQRVTEQSLG VPSAYASFAI PLGATSKMDG CAAVYPAVAA IFVAQFYGID LSIMDYVLIM
 IVSVLGSAAAT AGTTGATVML TLTLSTLGLP LAGVGLLLAI EPIIDMGRTA TNVTGQALVP
 AIVAKREGIL DQDVWDAAEK GGAAIEMATV SEKETEPAEV RS

> RXA01094 (1-948, translated) 316 residues
 MTLATIPSPQ QGVWYLGPIR IRAYAMCIIA GIIIVAIWLTR KRYAARGGNP EIVLDAAIVA
 VPAGIIGGRI YHVITDNQKY FCDTCNPVDA FKITNGGLGI WGAIVLGGGLA VAVFFRYKKL
 PLAPFADAVA PAVILAQGIG RLGWNFNQEL YGAETTVPAW LEIYYRVDEN GKFAVPTGTS
 TGEVMATVHP TFLYELLWNL LIFALLMWAD KRFKLEHGRV FALYVAGYTL GRFWIEQMRV
 DEATLIGGIR INTIVSAVVF AGAIIVFFLL KKGRETPEEV DPTFAASVAA DAVASPDRKP
 LPKAGEGIDG ETPSTR

> RXA01135 (1-324, translated) 108 residues
 VTHILFDSRR FLQLGAFASL STALAGAARY VTSTSNNEPA DNTPLTIGYV PIAGSAPIAI
 ADALGLFKKH GVNVTLLKYS GWSDLWTAYA TEQLDVAHML SPMTVAIN

> RXA01141 (1-462, translated) 154 residues
 VNSAADLKGM VLGIPEFYSV HALLLRDYLV SNAVDPIADL ELRLLRPADM VAQLTVEGID
 GFIGPGPFNE RAISNGSGRI WLLTKQLWDK HPCCAVAMAK EWKAEHPTAA QGVNLAALEEA
 SAILSNPAQF DSSARTLSQE KYLNQPATLL DGPS

> RXA01142 (1-420, translated) 140 residues
 TRTHLEQVGL TDAAERRPAR LSGGMQQRVG IARAFADIPP IMLLDEPFGA LDALTRRELQ
 LQLLNIWEAS RRTVVMVTHD VDEAILLSDR VLVMSKSPEA TIITDIPVNL PRPRHELSED
 ASVEAETAL RKRMLHLEH

> RXA01164 (1-1575, translated) 525 residues
 VTLFVRLALA AVGGFLVFAS NEPIGWFWAG IVGTALFFIS LAPWDLGVPQ KRRKKNEPVP
 FLQQMSTGPT VVQGMLLGFV HGLVTYLQLL PWIGEFVGS PYVALSVVEA LYSIALGAFG
 VLIARWRDWK VLLFPAMYVA VEYLRSSWPF DGFAWVRLAW GQINGPLANL AALGGVAFVT
 FSTVLAAGV AMVIISKRL AGAIITASVI AIGAVSSLYV DRNGTSDESI EVAAIQGNVP
 RMGLDFNAQR RAVLANHARE TLKLDEQVDL VIWPENSSDV NPFSDAQARA IIDGAVEHVQ
 APILVGTITV DEVGPRNTMQ VFDPVEGAEE YHNKKFLQPF GEYMPFREFL RIFSPYVDSA
 GNFQPGDGTG VVEMNAANLG RAVTVGVMT C YEVIFDRAGR DAIANGAEFL TTPTNNATFG
 FTDMTYQQLA MSRMRAIEFD RAVVVAATSG VSAIVNPDGS ISQNTRIFEA ATLTESIPLK
 DVTITAAARVG FYVELLLVII GVLAGLFAIR MNSRSKSAKG SARPA

> RXA01168 (1-720, translated) 240 residues
 RTATPDVHVL IVDDNSPDGT GERADKLAAD DDHIFVLHRE GKGGCLCAEYM AGFQWGLERD
 YQVLCEMDAD GSHAPEQLHL LLAEITNGAD LVIGSRYVPG GRVVNWPKNR WLLSKGGNVY
 ISVALGAGLT DMTAGYRAFR REVLEALPLD ELSNAGYIFQ VEIAYRAVEA GFDVREVPIT
 FTEREIGESK LDGSFVKDSL LEVTKWGLKH RGGQAKELSK EMVGLLLNYEW KHFKKRNTWL

> RXA01185 (1-858, translated) 286 residues
 MTDPEPNSQGT PQICPTDPTT QALAVRGLTK SYGDATVVNN INLDIPKGAI YGIVGPNGAG
 KTTMLSMATG LLRPNKGTAW ISGFNVWEEP NDAKRSMGLL ADGLPIFDRL TGKELLTYVG
 ALRELDEGIV DQRSEELLEA LGLKEAAGKR VVDYSAGMTK KILLAQALIH NPKVLILDEP
 LEAVDPVSGR LIQQILKNFA QTGGTVVLS HVMELVEGLC DHVAIINRGV VEIAGHVNEV
 RRGSRYSRMSS LMRLKALLFK RGHYLGWVRP KAIKAKAKIRT RIGLSK

> RXA01188 (1-1104, translated) 368 residues
 MMNGVVQPQE HLDATLIAAD FHGNPENS GD RKERLNFQGW KYALNRTVRD VFPGDLLDLA
 ALLTFFSILS IAPAVLLGYS VITIFLASDS TEILNLVRDE VNQYVPEDQS HVVNGVIDSI
 AGSAAAGQVG VAVGVITALW TSSAYVRAFS RCANAVYGRS EGRTLIKRW A MLLFLNLALL
 LGIILVSW VLNETLVMGI FAPIAEPLHL TNVLSFLTDR FMPIWIWVRF PVIVGVLMIF
 VATLYYWAPN ARPWKFRWLS LGSFLAIVGI LLAGVGLNFY FTLFAAFSSY GAVGSLLAVF
 IALWVFNICL IIGLKIDVEI SRAKQLQAGM PAEDYSLVPP RSIEKVAKMK QRQQLMDQA
 AAIREESN

> RXA01245 (1-1767, translated) 589 residues
 ASWVTTLGLG GFHLDFWWEL ALLVTIMLLG HWLEMRALGA ASSALDALAA LLPDEAEKV
 DGTTRTVAIS ELAVDDVVLV RAGARVPADG TIMDGAAEFD EAMITGESRP VYRDTGETTV
 AGTVATDNTV RIRVEATGGD TALAGIQRMV ADAQASSRA QALADRAAAL LFWFALITAL
 ITAVVVTIIG SPDDAVVRVAV TVLIIACPHA LGLAIPLVIA ISSERAACKSG VLIKDRMALE
 HMTIDVVLV DKTGTLTEGA HAVTGVPAT GIAEGELLAL AAAAEADSEH PVARAIVTAA
 AAHEASQRQ LRATGFTAAS GRGIRATVDG AEILVGGPNM LREFNLTPG ELADITGSWA
 QRGAGVLHV V RDGEIIGAVA VEDKIRPESR AAVRALQARG VKVAMITGDA TQVAQAVGKD
 LGIDEVFAEV LPQDKDTKVT QLQERGLSVA MVGDGVNDAP ALARA EVGIA IGAGTDVAME
 SAGVVLASDD PRAVLSMIEL SHASYRKMVQ NLVWATGYNI VAVPLAAGVL APIGVLLPPA
 AAAILMSLST IIVALNAQLL RRIDLDPAHL APTDGKEEKA AVSSAAPVR

> RXA01247 (1-234, translated) 78 residues
 VAAATDATPE GPTYQVTGM TCGHCADNVT EAVSALPQVD DVQVDLIAGG VSIVTVTGSV
 PLETVHRAIE ETGYTVLS

> RXA01285 (1-543, translated) 181 residues
 PQTSIAPEGI RYVDLIARGR APYQSLIQW RTSDEDAVAQ ALASTNLTEL AARLVDELSG
 GQRQRVWVAM LLAQQTPIML LDEPTTFLDI AHQYELLELL RAFNEAGKTV VTVLHDLNQA
 ARYADHLIVM KDGHVHATGT PEEVLTAEMV QGVFGLPCII SPDPVTGTPT VVPLSRSRAG
 A

> RXA01289 (1-1044, translated) 348 residues
 MTAVAVEKQK ETSISKNLGR RRALGILGIV VALGALIVLS IAVGANPLSF SSVWQGFTHA
 DSSEASIIWV SMRIPRTL VG IVTGAAFGVA GALIQALTRN PLADPGILGV NAGAGFAVTV
 GVGFFGLSSV TGYIWFALG AAAATLLVYF IGASTSGSVN PVALVLAGVA LAAVLGGVTS
 FLTLIDPETF ESIRNWNLGS VARTDLSDTM TVLPFLAVGL AIALLLSGAL NSIALGDDLA
 ASLGTKVMRT RVLGIISVTL LAGGATALTG GIGFVGLMVP HVVRWVVGPD QRWIITFSAL
 CAPVLVLGAD ILGRIIARPG EIEVGIVTAV IGAPVLIALV RRRKASGL

> RXA01290 (1-1164, translated) 388 residues
 VVFNISRTD ETPVAASEPV ESTRPVSEAS TSPALNPGYH AVSVQRRRFS FRIPARLMV
 SLILFAIALC SATWAITMGD YPLSLGQVIN ALAGTGEKFQ LLVVREWRLP VAIAAVVFGA
 LLGIGGAIFQ SITRNPLGSP DVIGFDAGSY TAVVLVILVL GNTHYWSIAF AAIVGGIVTA
 FAVYVLAWRK GVQGFRLIIV GIGVSAMLSS VNAYLITRAD VEDAMVVGFW SAGSINRITW
 QSLPLSLVIA AVIIVAAIVL ARSLRFMEMG DDVATTLGVK TNSTRALIV VGVATSALVT
 AAAGPISFIA LVAPQLARRL TKTPGVSLVA AAAMGSALLS CAHLLSLIIS SFYRTIPVGL
 LTVSIGGCYM IWLLLRETRR QYRTGTIR

> RXA01297 (1-798, translated) 266 residues
 MGYVGMVLAI LFIGLPLVFI VLTSFKQQSE IYTPVTFWP SEFNFDNYAN VFERVFPFLNY
 FRNSIIITVI LCLVKIILGV ISAYALSILR FPGRNLVFL VISALMVPSE VTVISNYALV
 SQLGWRDTYQ GIIVPLAGIA FGTFLMRNHF MSIPSELIEA ARMDHCGHFR LLWKVLLPIS
 MPTLVAFSMI TVVNEWNQYL WPFLMAETDN SATLPIGLTM LQNNEGVSNW GPVMAATIMT

MLPVLVMFLA LQEYMIKGLI SGA VKG

> RXA01298 (1-393, translated) 131 residues
 FVWKNLGYSF VIYLAALQGL NKDLSEAAPV DGASAWTRFW KVTLPQLRPT TFFLSITVTL
 NSVQVFDIIH TMTRGGPLGN GTTTLVYQVY TETFTNYRAG YGATIATILF LLLLIITVIO
 VRYMDKENKQ K

> RXA01303 (1-1335, translated) 445 residues
 VTQLNTKGVV LQGWDPEDPE HWDSKIAWRT LWITTFSMII GFCVWYLVSA IAPLLNRIGF
 DLSAGQLYWL ASIPGLAGGL IRLIYMFLPP ILGTRKLVGI SSGFLFLIPMF GWFLAVQDSS
 TPYWLLTLA ALTGIGGGVF SGYMPSTGYF FPKAKSGTAL GIQAGIGNLG VSIIQFMGPW
 VMGFGLLGIG FLTPQRTIEG TTVFVHNAAI VLVPTILAA VLSFLFLKDV PVTANFRQQI
 DIFGNKNTWI LSIIYLMTEG AFAGFAAQFG LIINNNEGIA SPMAETYPAE MLHAGATFAF
 LGPLIGALVR AAWGPLCDRF GGAIWTFVGG IGMTIATAAA AIFLSRAETP DDFWPFLWSM
 LALFFFTGLG NAGTFKQMPM ILPKRQAGGV IGWTGAIGAF GPFIVGVLLS FTPTVAFFWG
 CVVFFIIATA LTWIIYARP N APFPG

> RXA01323 (1-2265, translated) 755 residues
 MAQTPAKIPA ALNFIDVDLG VTGMTCTSCS ARVERKLNKL DGVEATVNYA TESAQVSYDP
 SKVSPEQLIK TVEDTGYGAF TMASAAAEE EDNAPADSGQ SRIDAARDHE AADLKHRVIV
 SALLSVPVVL VSMIPALQFN NWQWAVLTLV TPIFFWGGSP FHKATWANLK RGSFTMNTLV
 SLGTSAADLW SLWALFIENA GHPGMKMEMH LLPSASTMDE IYLETVAVVI TFLLLGRWFE
 TKAKQSSEA LRKLLDMGAK DAVVLRDGAE VRVPVNQLKL GDVFITRPGE KIATDGEVDE
 GSSAVDESML TGESIPVEVT KGSKVTGATL NTSGRLMVKV TRIGADTTLS QMAKLVTDAQ
 SKKAPVQRLV DQISQVFVPV VIVIAIATLI AHLVFTDAGL APAFTA AVAV LIIACPCALG
 LATPTALLVG TGRGAQLGLL IKGPEILEST KKVDITVLDK TGTVTGTMS VTDVTAINYS
 ETEILEFAAA VESASEHPIA QAIKAAAEHE QVTDFQNTAG QEVTVGVVRGH EVRVGRPSST
 LIDALLHPFQ HAQKIGGTPV VVTIDGVDSG IITVRD TVKD TSAE AIRGLK ELGLTPILLT
 GDNEGAAKSV AA EVGIDQVI ANVLPHEKVQ NVEALQAQ GK NVAMVGDGVN DAAALQAQDL
 GLAMGAGTDV AIEASDITLM NNDLRS AVDA IRLSRKTLGT IKGNLFWAFA YNVALIPVAA
 IGLLNPMLAG IAMA FSSVFV VSNSLR LRGF KARSN

> RXA01338 (1-1878, translated) 626 residues
 MLFIRSF DGI ITVAALVAIA IHLILWLALD LDGLAKNWPL IAIVIVGGIP LMWDVLKSAI
 KTRGGADTLA AVSIITSVLL GEWLVA AIIIV LMLSGGEALE EAASRRASGT LDALARRAPS
 TAHRLLGATI LDGTEEI AVE EITVGDLVAV LPHELCPVDG EIVAGHGTMD ESYLTGEPYV
 VSKSKGSQAM SGAVNGDTPL TIVATKLAHD SRYAQIVGV L HEAENNRPEM RRMADRLGAW
 YTVIALALGG LGWIVSGDPV RFLAVVVVAT PCPLLI AVPV AIIG AISLAA RRGII VKNPG
 MLENASGVKT VMFDKTGTLT YGRPVITDIH TAPGVEEDTV LALAASVERY SRHPLADAIR
 EGAKARELHL PDVVEV SERP GQGLTGT VGE HLVRITNRRS TLEIDPDSKN YIPVTSSGME
 SVVLVDDKYA ALIRLRDEPR ASASEFIAHL PKKHKVDKLM IISGDRASEV RYLADKVGID
 EVHAEASPED KLNIVNRHNE HGATMFLGDG INDAPAMAVA TVGVAMGADS DVTSEADAV
 ILDSSLERLD DLLHISARMR RIALQSAGGG MALSVIGMIL AVFGFLTPLM GAIFQEVIDV
 LAILNSARVA LPRGAISDFD TQEKVS

> RXA01395 (1-1086, translated) 362 residues
 MAVMAYQPAD NRYDDMIYRR VGNSGLKLPA ISLGLWHNFG DDKPLSTQRS IIHRAFRDGV
 THFDLANNYG PPAGSAETNF GRILREDLKS HRDELISSK AGWDMWPGPY GFGGSRKYL V
 SSLDQSLTRL GLDYVDIFYH HRPDPDTPLE ETMYALRDIV ASGKALYVGI SSGPELTAE
 AA EFMAEEGC PLLIHQPSYS IINRWVEEPG DDGENLLQSA ANNGLGVIAF SPLAQGLLTD
 KYLDGIPEGS RASQGSXXX XXLNVNIDX VXXXXXXXXXX TGQSFXKXK CWVVAQPRKV
 RRRITVTSAL IGASSVEQLD NSLDSLNNLE FSDAELEAID EISHDAGINI WAKATDSKTR
 EN

> RXA01411 (1-327, translated) 109 residues
 FIAQVMLGIG AVTANCVTSV MMAEVFQEV T RGTSAGITYN VTYAIFGGSA PFISTALVSW
 TGSPLAPAVY MIIIALFAFT ASRFIPETSP VFVTATPAIK APKVLVNPG

> RXA01454 (1-267, translated) 89 residues
 MMLIVAFLIA LVGHYLMGGI RAGNQMTGQK SFVSRGARTQ LAVTAGLWML VKVAGYWLD R
 YDLLTKENST FTGASYTDIN AQLPAK IIL

> RXA01455 (1-462, translated) 154 residues
 VTWIFAIIAL VILIAPMSVG FYTDWLWFGF VDFRGVFSKV IVTRIVLFEVI FALIAGFVTW
 LAGYFVTKLR PDEMSAFDTQ SPVYQYRQMI ENSLRRVMVI IPIFVALLAG LIGQRSWRTV
 QMWLNQDQDFG VSDQQFGLDY GFYAFDLPLM RLIA

> RXA01625 (1-201, translated) 67 residues
 MAIKNYTVEG MTCGHCVSSV KEEVGEVAGV TAVDVTLETG AVQVTGEDFT DEAVKAAVVE
 AGYKVVA

> RXA01756 (1-1308, translated) 436 residues
 MKELELGEAR DVAATLEAMP IQEVIDQVER TSITKGAVLL RLLSKDRSLL VFDALGPRLO
 ADLIGAFQDA EVLDYFADLD PDDRVSLLE LPASIADELL RSLDPQEKQV TELVLGYAKG
 SVGRWMSPOV LLLFDDMSVA EVLDFVRNHA AEAETIYALP IVNRARQVMG VVSLRKLFA
 DPTLKVSEIM VRPVSVLASA DIEETARWFL QLDLVAMPVV DESNMLLGVL TFDDAQDIVE
 QADSEDSARS GGSEPLQPY LSTPIRKLK SRIVWLLVLA VSAILTVQVL DIFEATLVEA
 VVLALFIPLL TGTGGNTGNQ AATTVTRALA LGDVRKSDVF RVLGREIRVG LMLGALLGAV
 GFVIASLVYG MPVGTVIGLT LLAVCTMAAS VGGVMPIIAK AIGADPAVFS NPFISTFCDA
 TGLIIYFAIA KLVVGI

> RXA01808 (1-1119, translated) 373 residues
 MRGGAPARTS KPGFRLEAAE ALIAEVPAPR DKVELMAFSK SRQGRVIEL EDATVATPDD
 RILVEDLTWR LAPGERIGLV GVNGSGKTTL LRTLAGEQPL QAGKRIEGQT VKLGWLRQEL
 DDLDSLRLI DCVEDVASV MMGDKQVSAS QLAERLGFSP KRQRTPVGDL SGGERRRLQL
 TRVLMAEPNV LLLDEPTNDL DIDTLQELLES LLDGWPGTMV VISHDRYLIE RVTDSWALF
 GDGKLTNLP GIEEYLQRA AMAAAEDSGV LNLGAATQAG TFSAAEQAA TSVESGSISS
 QERHRITKEM NALERKMGKL DQQMDKLNQQ LADAAEAMDT IKLTELDTKL RAVQEEHGE
 EMQWLELGE IEG

> RXA01822 (1-582, translated) 194 residues
 MARQNSNTGG LRLVLVGIGT GAFLGAARDF FMVRADITGA STVQLWSAGS LSGRDWNHAL
 LVLISCAVIV PALCIIVRRL RLMEMGDDAA GALGISVERT RLIAILLAVL LVGIATAAAG
 PIAFIALAAP QIARALARED GVLVAASISI GSGLLVAADC LEQHVDTLH TPVGLVTSLL
 GGVYLMWLLS RKEA

> RXA01890 (1-720, translated) 240 residues
 MASIVFENV T RKYSPGARPA VDKLNLEIAD GEFLVLVGPS GCGKSTSLRM LAGLEPIDEG
 RLLIDGKDAT ELRPQDRDIA MVFQSYALYP NMTVRDNMGF ALKNQKVAKA EIEKRVAEAS
 RILQLDPYLD RKPAALSGGQ RQRVAMGRAI VREPSVFCMD EPLSNLDAKL RVSTRAEISG
 LQRRMGVTTV YVTHDQVEAM TMGDRVAVLL LGVLQQVDTN QNLYDYPANA FVASFIGSLP

> RXA01900 (1-1299, translated) 433 residues
 MTTAVDQNSP PKQQLNKRVL LGSLSGSVIE WFDFLVYGTV AALVFNKMYF PSGNEFLSTI
 LAYASFSLTF FFRPIGGVIF AHIGDRIGRK KTLFITLMLM GGGTVAIGLL PDYNAIGIWA
 PILLMFLRIL QGIGIGGEWG GALLLAYEYA PKKQRGLYGA VPQMGISLGM LLAAGVISLL
 TLMPEQFLT WGWRIPFVGS ILLVFIGLFI RNGLDETPEF KRIRDSGQQV KMPLKEVLTK
 YWPAVLVSIG AKAAETGPFY IFGTIYIYAY TNFLNIRDNI VLLAVACAAL VATIWMPLFG
 SFSDRVNRV LYRICASATI VLIVPYLVL NTGEIWFALFI TTVIGFGILW GSVNAILGT
 IAENFAPEVR YTGATLGYQV GAALFGGTAP IIAAWLFEIS GGQWVPIAVY VAACCLLSVI
 ASFFIQRVAH QEN

> RXA01939 (1-603, translated) 201 residues
 STSGTDLTSL SHKEIFQMRR KLQVVFQNPY GSLDPMYSIY RCIEEPLTIH KVGGRKARE
 ARVVELDMV SMPRSTMRRY PNELSGGQRQ RIAIARALAL NPEVIVLDEA VSALDVLVQN
 QILTLLAELQ QELKLTLYLF THDLAVVRQT ADDVVVMQKG RIVEKGRD TD IFNDPQQHYT
 RDLINAVPGL GIELGTGENL V

> RXA01972 (1-594, translated) 198 residues
 VATGLLSAIG LFIATNIDDI IVLSLFFARG AGQKGTTLRI LAGQYLGFMG ILAAAVLVTL
 GAGAFPLPAE IPYFGLIPLA LGLWAAWQAW RSDDDDDDDA EIAGKKVGVL TVAGVTFANG
 GDNIGVYVPV FLNVDTAAVI IYCIVFLVLV AGLVLLAKFV ATRPPIAEVL ERWEHVLFP

VLIGLGIFIL VSGGAFGL

> RXA01986 (1-618, translated) 206 residues
 MASTFIQADS PEKSKKLPL TEGPYRKRLF YVALVATFGG LLFGYDTGVI NGALNPMTRE
 LGLTAFTEGV VTSSLLFGAA AGAMFFGRIS DNWGRRTII SLAVAFFVGT MICVFAPSFA
 VMVVG RVLLG LAVGGASTVV PVYLAELAPF EIRGSLAGRN ELMIVVGQLA AFVINAIIGN
 VFGHHDGVWR YMLAIAAIPA IALFFG

> RXA01995 (1-654, translated) 218 residues
 MDIRQTINDT AMSRYQWFIV FIAVLLNALD GFDVLAMSFT ANAVTEEFGL SGSQLGVLSS
 SALFGMTAGS LLFGPIGDRF GRKNALMIAL LFNVVGLVLS ATAQSAGQLG VWRLITGIGI
 GGILACITVV ISEFSNNKNR GMAMSIYAAG YGIGASLGGF GAAQLIPTFG WRSVFAAGAI
 ATGIATIAATF FFLPESVDWL STRRPAGARD KINYIARR

> RXA02033 (1-789, translated) 263 residues
 MPLSGKIGGF IVAVVFVLA LSFITWTFDP VQAFPQERLE GSSLRHLLGT DRYGRDVLSQ
 IMVGSRVTL VGIIAVAIAA LIGTPLGIAA GMRRGMVETF VMRGADLMLA FPALLLAIIS
 GAVFGASTWS AMVAIGIAGI PSFARVARAG TLQVTSQDFI AAARLSKVSS ARIALRHILP
 NITSMLIVQA SVAFALAILA EAALSFLGLG TTPPDPSWGR MLQTAQASIG VTPMLAVWPG
 AAIALTVLGF NLFQDGLRDA IDP

> RXA02034 (1-966, translated) 322 residues
 VSKTIAWTVL RYTLTFVIAS IIIFVLIRVI PGDPAVALG ITATPEAIAA LQSQLGTDQP
 LFQQYFSWIG GMLTGDFGTS LSSGQDLSP IFDRLQVSLI LVGCSIVLSL LIAIPLGVLS
 ARRGVVISG ISQIGIAIPS FLAGILLVAV FAVGLGWLP NGWIPPSNF GGFLARLILP
 VLALTAVQAA ILTRYVRSV MDVMGQDFMR TARSKGMSFN RALIIHGLRN AALPVLTVTG
 LQLTTLVIGA VVIEQVEVIP GIGSMLESV SNRDIAVQS IVMLLVAFITL LVNLVVDLLY
 QVVDPRVGAV GVASTKVP GS VA

> RXA02035 (1-1509, translated) 503 residues
 MKITRGLLPS LLLASTIVVS SCSAGSTAYQ QPPAVDQSSI VIATTAAAS LDFTNAAGAA
 IPQAMMSNIY EGLVRIDAEG EIQPLLATSW DISDDRTEYI FHLREGVLFS NGDPFNADSA
 KFSIDRVKTD WTNGLKSGMD VVESTVIDD HTLKVSLVRP SNQWLWSMGT AIGAMTEGG
 VDKLATDPVG TGPYTVTHWA PGRAIGFGAR ADYWGQKPLN DAATIRYFSD ATASTNALQS
 GDVDVIWAMQ APEQLATLQE YTVEVGTTNG EMLLSMNNQR APFDDVRVRQ AVMEFIDRQA
 VIDTALEGYG TDTGGVPVPP TDPWYEKSTM YPYDPDRARA LLEEAGAEGT RITMSIPSLP
 YAAQASEILY SQLRDVGFDV VIESTEFPV WLAQVMGQKD YDMSLIAHVE PRDIPTLFSP
 NYLGFDDTE TQALLAEADS SANEVELMQQ AVDRIMEQAV ADNLNMVANI VVMSPEITGI
 DPNVVSAGLE LSLIGRKESG VAQ

> RXA02062 (1-1170, translated) 390 residues
 MRVGMMTREY PPEVYGGAGV HVTETLRFMR EIAEVDVHCM GAPRDMEGVF VHGVDPALES
 ANPAIKTLST GLRMAEANN VDVVHSHTWY AGLGGHAAAR LHGIPHVATA HSLEPDRPWK
 REQLGGGYDV SSWSEKNAME YADAVIAVSA RMKDSILAAY PRIEPDNVRV VINGIDTELW
 QPRPTFDDAE DSVLRSLGVD PQRPIVAFVG RITRQKGVEH LIKAAALFDE SVQLVLCAGA
 PDTPEIAART TALVEELQAK REGIFWVQDM LGKDKIQEIL TAADTFVCPS IYEPLGIVNL
 EAMACNTAVV ASDVGGIPEV VVDGTTGALV HYDENDVETF ERDIAEAVNK MVADRETAAK
 FGLAGRERAI NDFSWATIAQ QTIDVYKSLM

> RXA02068 (1-1119, translated) 373 residues
 IFVPMRLIAA IEPKDITLVT GSVSLRTRFV RTGELQVMGD IVGAKVHTDD PELQQFHGRA
 VEIADVELEL SRTDWTITR VAVLGERPKF GRRPVLHTVP WSHIHGITAG GVGESNHTAE
 LIAGFEDMRP ADVAKQLYQL PTAQRTEVTE ELDDEKLADI LQELSEDROA ELIEELDIER
 AADILEEMDP DDAADLLGEL PDDKADVLLD LMDPEESAPV RRLMDFSPDT VGALMTPEPL
 IMPSTTVAE ALAMARNPDL PTLASLIFV VRPTATPTG KYLGCVHLQK LLREPPSSLI
 GGILDPDLPP LYADDSQETA ARFFATYNLV CGPVLNENRH LLGAVAVDDL LDHMLPEDWR
 DAGIRPGKEH THG

> RXA02079 (1-615, translated) 205 residues
 MSEAFDATKV RKAULTVALL NFAYFFVEFF IALSAGSVSL LADSVDFLED TSINLLIFIA
 LGWPLARRAV MGKLMIAVIL APAFAFAWAA IQRFSAPQAP EVFPIIVASL GAVVINGASA

IIISRVQRHG GSLGQAAFLS ARNDVLINIA IIMMALITAW TTSGWPDIL L GCFIILLALH
AAHEVWEVSE EERLASKALA GEAD

> RXA02096 (1-1317, translated) 439 residues
MGLDVSDEQI EHAARLAQAH DFIDRLPNKY EEVIGERGLT LSGGQRQRIA LARAFLAHPK
VLVLDDATSA IDASTEDRIF QALREELHDV TILIIAHRHS TLELGDRVGL VEDGRVTALG
PLSEMRDHAR FSHLMALDFQ DSHDPEFTLD NGSLPSQEQL WPEVSTKQY KILAPAPGRG
RGMSMPATPE LLAQIEALPA ATEETRVDAG RLRTSTSGFK LLSLFKQVRW LVVAVIALLL
VGVAADLAFP TLMRAAIDNG VQAQSTSTLW WIAIAGSVVV LLSWAAAAIN TIITARTGER
LLYGLRLRSF VHLLRLSMSY FERTMSGRIM TRMTTIDIDL SSFLQSGLAQ TVVSVGTLLG
VVTMLAITDA QLALVALSVV PIIIVLTLLF RRISSRLYTA SREQASQVNA VFHESIAGLR
TAQMHRMEDQ VFDNYAGEA

> RXA02119 (1-1641, translated) 547 residues
MTETLVVNGL AGGYGHRTLF NDVNLTVAAG DVVGVVGVNG AGKSTFLKIL AGVEKPLAGT
IALSPADAFV GYLPQEHRT SGETIAVYIA RRTGCQAATT AMDDTAEAFG ADPDNAALAD
AYAEALDRWM ASGAADLDER IPIVLADLGF ELPTSTLMG LSGGQAARVG LAALLLSRFD
IVLLDEPTND LDLDGLEQLE NFVQGLRGV VLVSHDREFL SRCVTTVLEL DLHQNSHHVY
GGGYDSYLEE RAVLRQHARD QYEEFAEKKK DLVARARTQR EWSSHGVRNA IKRAPDNDKL
RKKAASSE KQAKQVRQME SRIARLEVE EPRKEWKLOF SVGKASRSS VVSTLNDASF
TQGDFTLGPV SIQVNAGDRI GITGPNAGK TLLRGLLGN QEPSTGTATM GTSVAGIEID
QARALLDPQL PLISAFEKHV PDLPISEVRT LLAKFGLNDN HVERDVEKLS PGERTRAGLA
LLQVRGVNVL VLDEPTNHL DLEAIEQLEQA LASYDGVLLL VTHDRRMLDA VQTNRRWHVE
AGEVREL

> RXA02220 (1-2676, translated) 892 residues
VSSPLPAAVT SKPAHALSSD EVLENLGVQD TGLTSAEATQ RLEANGPNEL PQTPPETVWQ
RLFRQVNDPM IYVLIAAAVL TAFLGHWTDT IVIGAVVIIN MMVGFIQEGK AADALASIRN
MLSPESAALR DGVEHKKIDAA ELVVGDVVKL SAGDKVPADL RMLAATNLHI EESALTGEAE
AVVKGTDPEV ADAGIGDRTS MAFSGTLVLT GSGTGVVTAT GAGTEIGHIT TMLADVDSVD
TPLTRSMKKF SSALAIVCVF LAILMLVVAG LVHHTPLEEL ILSAIGFAVA AIPEGLPAVI
AITLALGVQK MAARNAITRR LNSVETLGSV TTICTDKTGT LTRNEMTVRA IATGTSLYDV
SGAGYEPLGE IRLKDGEQVS KQDFPDLYAM ALVAANVND EIIYQEDGMWR LSGETPDGGI
RAFAMKTNAE ILTRTAEVPE DSAYKYMATL HTIDGANTML VKGAPDRLLD RSAQQRNGEP
LDRPYWEQLI EDLASQGLRV LAAAYKELPH STSTITPEDV DQGELTFLGL YGIMDPPREE
VIEAMKVVSQ AGVRVRMITG DHSSTARAI A REVGIRGQNV LTGAETIAT DEELQGLVDN
ADLFVRTSPE HKLRVVRLQ ANGEVASMTG DGVNDAPALK QADVGVAMGI KGTEATKDA
DIVLADDNFA TIAGAVEMGR TIYDNLKAV VFMLPTNGAQ GLVIFIAMLL GWELPITALQ
VLWINLITAI TSLALSFEPA AEPGIMNRKP RNPKSGLIDA PSVLRIVYVS LLLGGATFWA
FLGARDAGID IDTARTIAVT TLAVSQVFYL LSSRYFEVSA LRKELFTTNP ISWLCIALML
ILQLAFVYLP FMQSTFDATA LTLRDWVMP L VFGVVVFAV ETEKFIRRLK AS

> RXA02222 (1-375, translated) 125 residues
LGRPPPGDVH TLLDDIGAE SEADKVPIEW QNALTAKADRY ANRQHMSQAR LYRQLTSDVG
EGFTEEAAQY AIENVNADWN ANALVKARNY QERQAMSVDR IYRQLTSEHG EGFTPEQAQY
AIDNL

> RXA02312 (1-1359, translated) 453 residues
LSNRHLQLIA IGGAIGTGLF MSGSKTISVA GPSVILVYAI IGFMFFVVR AMGELLANL
NYKSLRDAVS DILGPGAGFV TGWTYWFCWI ATGMADIVAI TGYTQYWWPE IPLWLPGVLT
IALLFALNLA AVRLFGEFMEF WFAIIKIVAI VSLIVVGLFM VVTAFESPNG TTAQFNNLIE
HGGFFPNGIT GFLAGFQIAI FAFVGIELAG TAAAETENPT KTLPRAINSI PIRIVVFYVL
ALAVIMMVTP WDQVRADNSP FVQMFALAGI PAAAGIINPV VITSAASSAN SGIFSTSRML
YGLSLEGAAP KRWSRLSKNL VPARGLTFSV ICLIPAVGLL YAGGTVIEAF TLITTVSSVL
FMVVWSYILV AYIVYRRNSP ELHKKSIKFM PGGVVMMAVV LVFFAAMLV LSLEPDTRAA
LIATPVWFII LGIGWLSIGG AKGAKHRSQI TSH

> RXA02313 (1-1221, translated) 407 residues
MRVAIVAESF LPNVNGVTNS VLRVLEHLKA NGHDALVIAP GARDFEEEIG HYLGFIVRV
PTVRVPLIDS LPIGVPLPSV TSVLREYNPD IHLASPFVL GGAAFAARQ LRIPAIAYQ
TDVAGFSQRY HLAPLATASW EWIKTVHNM QRTLAPSSMS IDELRDHGIN DIFHWARGVD

SKRFHPGKRS VALRKSWDPS GAKKIVGFVG RLASEKGVVER LAGLSGRSDI QLVIVGDGPE
 AKYLQEMMPD AIFTGALGGE ELATTYASLD LFVHPGEFET FCQAIQEAQA SGVPTIGPRA
 GGPIDLINEG VNGLLLDVVD FKETLPAAAE WILDDSRHSE MCAAWEVGVK DKTWEALCTQ
 LLQHYADVIA LSQRIPLTFF GPSAEVAKLP LWVARALGVR TRISIEA

> RXA02344 (1-678, translated) 226 residues
 MLNRMKSARP KSVAPKSGQA LLTLGALGVV FGDIGTSPLY SLHTAFSMQH NKVEVTQENV
 YGIISMVLWT ITLIVTVKYV MLVTRADNQG QGGILALVAL LKNRGHWGKF VAVAGMLGAA
 LFYGDVVITP AISVLSATEG LTVISPSFER FILPVSLAVL IAIFAIQPLG TEKVGKAFGP
 IMLLWFVTLA GLGIPQIIGH PEILQSLSPH WALRLIVAEP FQAFVL

> RXA02348 (1-1134, translated) 378 residues
 PIRVAWFCVV MPALILTYLG QGALVINQPE AVRNPMFYLA PEGLRIPLVI LATIATVIAS
 QAVISGAYSL TKQAVNLKLL PRMVIRHTSR KEEGQIYMPV VNGLLFVSVM VVVLVFRSSE
 SLASAYGLAV TGTLVLVSVL YLIYVHTTWW KTALFIVLIG IPEVLLFASN TTKIHDGGWL
 PLLIAAVLIV VMRTWEWGS RVNQERAELE LPMDFLEKL DQPHNIGLRK VAEVAVFPHG
 TSDTVPLSLV RCVKDLKLLY REIVIVRIVQ EHVPHVPPEE RAEMEVLLHA PIRVVRVDLH
 LGYFDEQNL P EHLHAIDPTW DNATYFLSAL TLRSLRPGKI AGWRDRLYLS MERNQASRTE
 SFKLQPSKTI TVGTELHL

> RXA02353 (1-468, translated) 156 residues
 MALLILAGLQ MIPKETYEAA RVDGATAWQQ FTKITLPLVR PALMVAVLFR TLDALRMYDL
 PVIMISSSSN SPTAVISQLV VEDMRQNNFN SASALSTLIF LLIFFVAFIM IRFLGADVSG
 QRGIKKKKLG GTKDEKPTAK DAVVKADSAV KEAAKP

> RXA02354 (1-789, translated) 263 residues
 MTKRTKGLIL NYAGVVFILE WGLAPFYWMV ITALRDSKHT FDTTPWPTHV TLDNFRDALA
 TDKGNNFLAA IGNSLVISVT TTAIAVLVGV FTAYALARLE FPGKGIVTGI ILAASMFPGI
 ALVTPLFQLF GDLNWIGTYQ ALIIPNISFA LPLTIYTLVS FFRQLPWELE ESARVDGATR
 GQAFRMILLP LAAPALFTTA ILAFIATWNE FMLARQLSNT STEPVTVAIA RFTGPSSFEY
 PYASVMAAGA LVTIPLIIMV LIF

> RXA02394 (1-1311, translated) 437 residues
 MLSPAAVAAL ILVIGIVVLI IASVPVAIAI GLPSLFAAMA VLGPENAAQA VAQRMFTGTN
 SFTLLAIPFF VLAGLLMNSG GIATRLIDAA KVLVGRMPAS MANTNIAANG LFGAVSAAV
 ASASAVGTVM TPKMKEEGYS RAYAAVNVA SAPAGMLIPP SNTFIVYSLV SSTSIAALFM
 AGVGPGLLWI LACVIVGTWL ARKENYKREQ IHPTFKQSLV VLWRALPSLL MIVIVGGIL
 LGWFTPTESA AIAVVYCLVL GFYRTIKVG DLADILLKAT RTTSIVMLLI AVSAALSWVM
 AFAKIPQMIS DALLSVSDSK VVILLIMFI LLLIGTVMDP TPAILIFVPI FLPVVTELGV
 DPVHFGAMVV MNLSVGVITP PVGNVLFVGS QVAGLRVETV IRRLWPYLIA IIVALFVVVF
 VPQISIWLP TMGLMGG

> RXA02402 (1-744, translated) 248 residues
 VSKTEEGRSA AIIYAFPTF ILLGAIIFI FPEPFIPLTN YINIFLTIIM FTMGLTLTVP
 DFQMVLRPL PILIGVVAQF VIMPFLAIV AKMFNLNPAL AVGLLMLGSV PGGTSSNVIA
 FLARGDVALS VTMTSVSTIV SPIMTPFLML MLAGTETA VD GGGMAWTLVQ TVLLPVIIGL
 VLRVFLNKWI DKILPILPYL SILGIGGVVF GAVAANAERL VSVGLIVFVA VIVHNVLYGY
 VGYLTGRV

> RXA02422 (1-435, translated) 145 residues
 VSTLISEPEV DKLRKRAKRS RRTIEWLAAA LLAPNLLLLA IFTYRPLLDN FRLSFFNWN
 SSPTSTFIGF DNYVEFFTRS DTLQVVLNTV IFTACAVIGS MVLGLLLAML LDQKLFG
 VRSMVFAPFV ISGAAIGGAF QFVFD

> RXA02438 (1-759, translated) 253 residues
 MTDLIQLREV SKKYGAFQAL NDINLNVVRAG EVTCVLGDNG AGKSTLIKIL SGLHPATSGE
 VIVAGDVVNF GSPRDALDAG IATVYQDLAV VGQMSVWRNF FLGQELTGRF GVLKQEMRR
 ITDEQLREMG IELRDVDVPV ASLSGGQRQV VAIARAIYFG ARVLILDEPT AALGVKQSGM
 VLRFIAAARD RGIGVIFITH NPHHAYLVGD HFILLNLGKQ VMDKSRAEVE LEELTLMSG
 GGELDSLSE LKR

> RXA02439 (1-1023, translated) 341 residues
 MTKIKSGEAS TSIVERALKR PELTSLLGAV LVFTLFMVVA PAFRSWDSMA TVLYASSTIG
 IMAVAVGLLM IADEFDLSTG VAVTTAALAA SMFSYNLWLN TWVGALIALV ISLAIGFFNG
 FLVVVKTIAS FLITLATFLM LQGINLAVTK LISGTVATPT IADMEGFPSA RAVFASSIPI
 FGVNIRITVF WWLLEFVIVGT FVLFKTRIGN WIFAVGGDEE AARAVGVVPR GVKIGLFMFV
 GFAAWFVGMH NLFLFDSIQA GQGVGNEFLY IIAAVIGGIS MTGGRGTVVG TMIGALIFGM
 TNQGIVYAGW NPDWFMFFLG GTLLLAVLLN HRFERFNKER S

> RXA02441 (1-657, translated) 219 residues
 MAELSVRNLT CTYGNHIALN NITARFPTGK ITALIGSNGS GKSTLLETIA GMLAPRSGSI
 NNLVPEIAFV PQRSHVSHNL PITIROTVSM GRWSAKKNWQ RLTAADCNIV DSCLDRLAIS
 GLADRPLGEV SGGQRQRALI AQGLAQQAPL LLLDEPLAAV DSHAASLIED VINQQRNQGT
 TIILATHDLD QAHQADQIIA LEKGIKPKR KATESIKKR

> RXA02442 (1-849, translated) 283 residues
 MKFFTDALIV PFDVSFISRA LVAGCLAAIL CSLIGTWVIL RRLTFFGDAM SHGLLPGVAT
 ASLLGGNLMF GAAISALIMS AGVVWTSRKS SLSQDVSIGL QFITMLSLGV VIVSHSDSHA
 VDLTSFLFGD ILGVRPSDIF IIAIATVLGG LTIFLFHRQF TALAFDERKA HTLGLNPRFA
 HLLMLALIAL ATVVVSFQVVG TLLVFGLLIG PPATAALLVQ DKASISLIMI VASLLGCAEI
 YLGLLISWHA STAAGATITL LSAAIFFATL LTKSAISRLN FTA

> RXA02447 (1-270, translated) 90 residues
 WVWLAEIIPV RMKGIGTGIS VFCGWINGV LALFFPALVS GVGITFSFLI FAVVGVIALA
 FVTKFVPETR GRSLEELDHA AFTGQIFKKA

> RXA02451 (1-1524, translated) 508 residues
 MNTDTTQDGV SPEPSDPHLG SEVAETHREK KFFGQPWGLA NLFGVEMWER FSFYGMQSIL
 AFYLYYSVTD GGLGMNQTAAL LSIVGAYGGF VYMTSLVASF IADRVLGSER TLFYSIIIVM
 LGHIALALIP GYTGLSIGLV LIGLGGGGV TAAQVVLGQL YSRDTRRDA GFSIFYMGVN
 LGGLFGLPLT NALGWGGGFH WGFGIAAVGM ALGLIQYVAM RKTITIGAAGH TVPNPLPKNE
 YARWIIIGAVV VVAAVVALIA TGIKLEWLS NITAAIALIA AIALLAQMYV SPLTTAAEKS
 RLLGFIPMEI GGVLFFAIFQ TQFTVLAVYS DTRLDRNFFG IDLPPGLINS FNPIFIIFIS
 GIFATLWTKL GAKQWSTAVK FGVANIVIGC ALFFFLPFAG GAENSTPMAL IIVVYFLFTI
 AELLSPVGN SLATKVAPEA FQSRMFAVWL MAVSMGTSLS GTLGGYYDPT DAGSEKVFPI
 TVGVAAIVLG AIVIAAKGWV LKKFIDVR

> RXA02491 (1-1254, translated) 418 residues
 MRVAMISMHT SPLQPGTGD SGMNVYILS TATELAKQGI EVDIYTRATR PSQGEIVRVA
 ENLRVINIAA GPYEGLSKEE LPTQLAAFTG GMLSFTREK VTYDLIHSY WLSGQVGWLL
 RDLWRIPLIH TAHTLAAVKN SYRDDSPTPE SEARRICEQQ LVDNADVLA VNTQEEMQDLM
 HHYDADPDRI SVVSPGADVE LYSPGNDRAT ERSRRELIGP LHTKVVAFVG RLQPFKGPQV
 LIKAVAALFD RDPDRNLRI ICGGPSGPN TPDYRHMAE ELGVEKRIRF LDRPPSELV
 AVYRAADIVA VPSFNEFGL VAMEAQASGT PVIAARVGGL PIAVAEGETG LLVDGHSPHA
 WADALATLLD DDETRIRMG EDAVEHARTS WAATAAQLSS LYNDIAIANEN VDGETHHG

> RXA02507 (1-1401, translated) 467 residues
 MSEQLQGVTH SESTPGKTPK RAALSSWIGS ALEYDFAVY GTAAALVLNH LFFPADTSPG
 IAILAAMGTV GVAYVVRPLG ALIMGPLGDR YGRKFVLMCL LFLIGASTFA VGCLPTFDQV
 GYLAPALLVL CRVIQGLSAS GEQSSAISVS LEHADERHRA FTASWTLHGT QFGTLLATGV
 FIPFTLFLSE DALMSWGWRV PFWLSAAVVL VAFLIRRGLE EPPAFRENKE AVAGAASPLA
 MTLRYHKAHV ARVAIAAMIN SVNIVFTVWA LSFATNIVGL DRSTVLLVPV VANLVALIAI
 PLSGMLADRI GRRPVFIMGA IGGGLAMNGY LGAIYSGNWT MIFFMGVLM GLLYSMGNV
 WPAFYAEMFP TSVRVTGLAL CTQIGFAVSG GFVPVIASAL AGDQGDQWMK VSIFVGVVVCV
 ISALVAMTAK ETKALTLDEI DALHTAGGEA ADLAAASKAS EAQLAAQ

> RXA02515 (1-756, translated) 252 residues
 MSTLEIRNLH AQVLPSDESA EPKEILKGVN LTINSGEIHA IMGPNNGSGKS TLAYTLGGHP
 RYEVTAGEVL LDGENILEME VDERARAGLF LAMQYPTIIP GVSVANFLRS AATAIRGEAP
 KLEWVKEVR TAQEALAIIDP EFSNRSVNEG FSGGEKKRHE VLQDLKPK FAIMDETDSG
 LDVDALRIVS EGINSYKQET EGGILMITHY KRILNYVKPD FIHVFANGQI VTTGGAELAD
 KLEADGYDQF IK

> RXA02562 (1-720, translated) 240 residues
MFLTQVSLLD HPESLPGYLS SLAIVEYLHE QPLEFRAPIT VITGENGVGK STLVEALAVG
MRLNPSGGSR HANFGREGDI VSSLHQSLKL VRRENPRDAF FFRGETMYNV ASYEEELMGE
KNMHDHLHKMS HGESVFAVID RRFNNQGGFFV LDEPEAGLSM LRQLELLGKL GNLARGGAQI
IMATHSPILL AIPGAEILEI TSSGVAKVNF EDAAVRAAR EFVADPRGTA AFLTAEEDHQ

> RXA02595 (1-651, translated) 217 residues
VIVVAMASIM ACLKAARLNN PMKILLLCWR DTTHPQGGGS ERYLERVGEF LADQGHEVVF
RTAGHTDAPR RSFRDGVRY SSGGKFSVYP KAWVAMMLGR VGIGTFISKVD VVVDTONGIP
FFGKFFSGKP TVLLTHHCHK EQWPVVGRVL AKVGWLIQS IAPRAYKTAP YVTVSEPSAE
ELIALGVDDQ RIHIVRNGVD PVPLHTPKLD RDGQHAV

> RXA02597 (1-1788, translated) 596 residues
LPEQDLTTLA NDWLQAFEKA TASSSPDEAA TAVVQLFEDE GYWRDLLAFT WNLTTAEGAD
EIAEMIRNTW PSSIFRNVEL KGEPADEGDG VTRVHFSCS ADFKCTGIVR LRNGKAWTLL
TSARELLEHP EPKGRNREM VVHGQNEETR NWTDRKNDRQ AALGVTEQPY TLIIGGGQGG
IALGARLKRL GVPALIIDKA SRPGDQWRSR YHSLCLHDPV WYDHLPIYPF PDHWPVFTPK
DKMGDWLEHY VGIMDLDYWT NTECLRASYN EDTKQWDVTV NRDGAESTLH PTQLVMATGM
SGSPNKPTLP GQDKFQGEIR HSSEHPGGDV DRDKNVVVLG ANNSAHDICA DLYSNGAKPV
MIQRSSTHIV RSDSLMREVF GLYSEDAVE AGIDTDTADL LFASWPYKVL PGVQKQAFDK
IREDDKEFYD KLENAGFLD FGDDDSGLFL KYLRGSGYY IDVGASELVA DGKIPVRSNV
SIEDVKENSV VLTDTGTELP DVIVLATGYG NMNNWVAQLV DQETADKVGW CWGLGSETTK
DPGPWEGELR NMWKPTNVDS LWFHGGNLHQ SRHYSRYLSM QLKARYEGMN TPVYSK

> RXA02605 (1-495, translated) 165 residues
VACPWAGTAA LNLAAKHPDQ FRQAMSWSGY LNTTAPGMQT LLRVAMLDTG GFNVNAMYGS
IINPRRFEND PFWMGGLAN TDVYISAASG LWSPQDDGVR VDHRLTGSVL EFMVAMTSTRI
WEAKARLQGL NPTADYPMY IHGWAQFNSQ LERTQGRVLD VMNAW

> RXA02614 (1-729, translated) 243 residues
MTATLSLKPA ATVRGLRKS YGTKEVLQID LTINCGEVTA LIGRSGSGKS TILRVLAGLS
KEHSGSVEIS GNPVAFQEP RLLPWKTVD NVTFLNRTD ISWSEAQERA SALLAEVKLP
DSDAAWPLTL SGGQAQRVSL ARALISEPEL LLLDEPFGAL DALTRLTAQD LLLKTVNTRN
LGVLLVTHDV SEAIADADHV LLLDDGAITH SLTVDIPGDR RTHPSFASYT AQLLEWLEIT
TPA

> RXA02616 (1-711, translated) 237 residues
LQKHTRGGKH RKQTTSPVTK GGVAFAVAT GAVSTAGAGG AVAAQASNQP VEVNFELTAN
DTTDLVAGSS APQILSIAEF KPVVNLGDQI VKTIQYNADR IQADLDARGP SVVRPAEGSY
TSGFGARWGT NHNGVDIANA IGTPILAAMD GTVIDAGPAS GFGNWWRLQH EDGTITVYGH
METVEVTVGQ TVKAGERIAG MGSRGFSTGS HLHFEVYPAG GGAVDPAWPL AERGITL

> RXA02627 (1-843, translated) 281 residues
DVTVESQPER VVALGWGDAE AALEFGVQPV GASDWLAFGG EGVGPWIEDS AYDEAPEIIG
TMEPEYEKIA ALEPDLILDV RSSGDQERYD KLSSIALTIG VPEGGDSYLT PRAEQVTMIA
TALGQAERGE EVNAEYEQLT ADIRAAHPGW PEKTAAVSA TATSWGAYIK GSNRVDTLDD
LGFQENPELA KQQPGDTGFS IKFSEETFGV VSDSLVVGFA IGMTPEEMAE QVPWQMLTAT
RDGRSFVMPE EISNAFSLGS PQSTRFALDA LVPLLEEHA E

> RXA02628 (1-405, translated) 135 residues
MLEGFRDFVL RGNVIELAVA VVIGTAFTAI VTAFSESIIN PLIASIGSTE VEGLGFHIRA
GNAATFVDFG AVITAAINFL IIAAIVFYVL VAPMKNLSET LAKRKGVEED ETPASIEAEL
LTEIRDLLQE QKRLQ

> RXA02650 (1-579, translated) 193 residues
MVNVTSKDAG ANVTPMSKKE KRRTVKQVVA LMAAIVVVIA SLDQIVKQIM LSWLEPGVPV
PIIGDWFRFY LLFNPGAAFS MGENSTWIF TTIQLSFVIG IAIYAPRIKH KWIAAGLALV
AGGALGNVLD RLFRDPSFFF GHVVDYISVG NFAVFNIAA SISCGVVVFL IGMFLEDREN
AQHAKATDEK DEA

> RXA02660 (1-639, translated) 213 residues
 MIIGVTLLVF IVMSFSPADP ARLALGESAS PEALEAYREA NGLNDPMMVR YFDFILGMLK
 GDGLTSSGGV AVTDIVARAF PITLQLTFWG LIIAVVVALI LGVIAALYRD RWPDQLIRVV
 SIAALATPSF WLAILLIQWL GTIPGAWGFF PALVTRWVPF SEDPATYFNN IALQRLRWQS
 PLQVLWPALF VPPWWKNWTR TTSQQSVQD PQN

> RXA02661 (1-219, translated) 73 residues
 VIGLRVGLSM GGAVIIEIIF NIQAMGQLIL DGVTRNDVYL VQGVTLTVAI AFIIVNIAVD
 LLYVLVNPRI RSI

> RXA02663 (1-1395, translated) 465 residues
 MAPILVFATV LVADAIVFEA SLSFINAGVK PPSPSWGNI L ADGKALLLSG AWWPTFFPGL
 MILLTVLCLN ILSEGLTDTL ASPKPKPVSA SAKKALKKEE SGEKEGSGIV LGHTTREETAN
 ASLLASLAAL STSENNNSNNR LIFDGNPTPL LEVRDLKISF PNAHGDIIV DGVNFTVAPG
 QTMGLVGESG CGKSITAMSI MGLLPPTAKI EGEILFDGKN LLDLKPDELN ALRGHEIAMI
 YQDALSSLNP SMLISAQMKQ LTRRGGRSA EELLELVGLD PKRTLQSYPH ELGGGQRQVR
 LIAMALTRNP RLLIADEPTT ALDVTVQQQV VDLLNELREK LGFAMIFVSH DLALVARLVH
 KLTVMYAGQV VEQGTREIL IDPRHEYTRG LLGSVLSIEA GVDRLYQVPG TVPSPKEFVA
 GDRFAPRSEF PELGLDQKPV LRPITGTEHA YAATDELLAA KGEQR

> RXA02664 (1-660, translated) 220 residues
 VGESGCGKST LARVMVGLQP VTSGEVLFGK KPMKPRGAQR KELGSSSVSVV FQDPATSLNP
 RMTVREQLLD PLRVHKVGDE ASRNQWVSEL ISMVGLPQSA LEVLPRQVSG GQRQVRVIAIAR
 ALALKPDIIV ADEPTSALDV SVRAQVLNLL LDLKTELGLG LVFISHDINT VRYVSDRIAV
 MLAGEIIEEN TTSEIFNNAQ QDYTRTLLEA TPSSLNKTRL

> RXA02684 (1-864, translated) 288 residues
 VLAUGLVLVF VVTWADSKL NRVDATPATQ VANTAGTNWL LVGSDSRQGL SDEDIERLGT
 GGDIGVGRD TIMVLHMPRT GEPTLLSIPR DSYVNVPGWG MDKANAAFTV GGPELLTQTV
 EEATGLRIDH YAEIGMGGLA NMVDAVGGE MCPAEPMYDP LANLDIQAGC QEFDGAAALG
 YVRTRATALG DLDRVVRQRE FFSALLSTAT SPGTLLNPFR TFPMISNAVH TFTVGEGDH
 WHLARLALAM RGGIVTETVP IASFADYDVG NVAIWDEAGA EALFSSMR

> RXA02728 (1-813, translated) 271 residues
 MAIVSLDNVT VSIEGKKLLD AVSLKAYPGE VLGLIGPNGA GKSTLLSVLS GDRLPDSGEV
 NVGGLDPATA AASDMARVRA VMLQDVSVAF SFLVWDVDEM GRRPWQKAST PEEDHEIIEA
 ALAATSVSHL AEREITTLTG GERARVALSR VLAQQTPIVL LDEPTAAMDI SHQEQTGLTA
 RALAAAGAAV IVVLHDLNAA AAYCDSIVCL SDGRVIASGS VDQVYSTETL SRVYGWPIRV
 DHSGKYVRVE PDRSEANLPS VLQVKNTVSP A

> RXA02750 (1-816, translated) 272 residues
 MAVLFSIMGA LILLVLYLVF LGKLQIDGLM VDLPSARD D VEGFVFNWVF SGILITSAIT
 VPQAALGVLV EDRTGGIKD FLVAPVSRTT LTVSYIFAAV IVAMTILIFE IVVGSIGLAI
 LGHFMSIAR VLELVVALLL LTLVFSIAIA FLITLVKSQG GMSALSSLVG TLAGFLSAAY
 IPPIALPEAV TNVLNLFPLFT PAGMLIRQIV VAPALDAISL PPEAFDIFQF GYGLKLEMFG
 EPVSTWVAVG IVASWGVVFG LIAAFKMKSV VR

> RXA02761 (1-201, translated) 67 residues
 MMDGINRRTT LITGYSLTTI SHVLIGIASV AFPVGDPLRP YVILTLVVVF VGSMQTFNLG
 SYLGYAL

> RXA02762 (1-285, translated) 95 residues
 MLSELFPLAM RGFAIGISVF FLWIANAF LG LFFPTIMEAV GLTGTFMFMA GIGVVALIFI
 YTQVPETRGR TLEEIDEDVT SGVIFNKDIR KGKVH

> RXA02769 (1-711, translated) 237 residues
 TVVPVYLAEL APLEIRGSLT GRNELAIVTG QLLAFVINAL IAVTLHGVID GIWRIMFAVC
 ALPAVALFLG MLRMPESPRW LVNQGRYDDA RRVMETVRTP ERAKAEMDEI IAVHSENNAA
 LPGVKQSSGQ ASGQVSSKHT HMSIGEVL SN KWLVRLLIAG IGVAVAQQLT GINAIMYYGT
 RVLEESGMSA EMAVVANIAF GAVAVIGGLI ALRNMRLDR RTTFIIGLSL TTFHLL

> RXA02795 (1-1095, translated) 365 residues
 IDVSLPERTA SAYPHELSSG QRQRALIAM LANDPDLIC DEPTTALDVV VQKQIVDLLL
 RLTKERGTA LFITHDLGLI ARTCERLLVM KSGETVERGD TEAILRSPAH SYTQQLLDAS
 ILDQPEIASD SGAPVVIDVE EASKSFKETT ALHKVSLAVR KGDLLGIVGG SGSGKTTLLK
 LIAGLDKPTT GTVAVTGGVQ MVFQDPQSSL NPRMKIKDIV AEPLLGWNAE EKTTRVAEVI
 TQVGLSPDVL DRYPHEFSGG QRQRISIARA LAIKPAILLA DEPVSALDVS VRKQVLDLLQ
 QLVEEYGITL VEVSHDLAVV RHLCTTVWVM EQGRVLEQGP IDSVYDHPQT EYTKELLDVAV
 PRLSL

> RXA02808 (1-258, translated) 86 residues
 FYFGILPVLA ESASHFGIEP VEMARASITG QPVHMQSPLV PAILLLVSLA NVNLGDHKKK
 VLWRACIVSI AMLAVALFIG VVPLSA

> RXA02863 (1-975, translated) 325 residues
 MKKSLIAIVA SALVLSGCTS DSSDSSGTSG TVETTSITTS VAAADGAFPR TVTLDDSSIT
 LESKPERIAV LTPEAASLVL PITGADRVVM TAEMDTADEE TAALASQVEY QVKNNGSLDP
 EQVVAGDPDL VIVSARFDTE QGTIDILEGL NVPVVNFSD AWGDIDAITK HLEIVGELVG
 EEDKAAEAIA EIDANRIDID KPATSPTVLT LMQRGPRQMV MPESAMLNGL IREAGGTPVV
 DSLGAVGTIT ADPEQVVAMA PEIIIIQDFQ GKGRNFANF LSNPALANVP AIENDKIFYA
 DVTVTGVTAG TDITGLQQV AEMLS

> RXA02864 (1-780, translated) 260 residues
 MPQLVEIRDL NVEFPSRHAV KNVSFSAPAG KVTALIGPNG AGKSTALSAI AGLVESTGEV
 MVGGSGVASK SAKARARLLS LVPQNTLRI GFSARDVVAM GRYPHRGRFA VETDADRRAT
 DDALRAINAL DIAEQPVNEL SGGQQQLIHI GRALAQDTAV VLLDEPVSA DLRHQVEVLQ
 LLRARANSQT TVIVVLHDLN HVARWCDHAV LMADGEVVSQ GDIREVLEPA TLSTVYGLPI
 AVRDDPETSS LRVIPHPNPF

>RXN00001 TRANSLATE of: rxn00001.seq check: 7420 from: 1 to: 1128
 MATVTFKASLSYPGAKEPTVKKFNLEIADGEFLVLVGPSCGKSTTLRMLAGLENTVDG
 AIFIGDKDVTHVAPRDRDIAMVFQNYALYPHMTVGENMGFALKIAGKSQDEINKRVDEAA
 ATLGLETFLEKPKKALSGGQRQVRAMGRAIVRNPOVFLMDEPLSNLDAKLVRVQTRTQIAA
 LQRKLGVTTVYVTHDQTEALTMGDRIAVLKDGYLQQVGAPRELYDRPANVFVAGFIGSPA
 MNLGTFSVKGDATSGHARIKLSPETLAAMTPEDNGRITIGFRPEALEIIPGESTDLSE
 PIKLDVEELGSDSFLYGLVGEGLGSSSEDVPESGQIVVRAAPNAAPAGSVFHHARIV
 EGGQHNFSASTGKRLP

>RXN00099 TRANSLATE of: rxn00099.seq check: 3872 from: 1 to: 1173
 VKNPRLIALAAIILTSFNLRTAITALAPLVSEIRDDLGVASLIGVLGMIPTAMFADAAAF
 ALPSLKRKFSTTSQLLMFAMLLTAAGQIIRVAGPASLLMVGTVFAMFAIGVTNVLLPIAVR
 EYFPRHVGGMSTTYLVSFQIVQALAPTAVPISQWATHVGLTGWRVSLGSWALLGLVAAI
 SWIPLLSLQGARVVAAPSKVSLPVWKSSVGVLGLMFGFTSFATYILMGFMQPMVGDPQL
 GAVLLGWWSILGLPLNILGPWLVTFTNCFPMVVIASVMFLIGNGGFCLAPDVAPWLWAT
 LSGGLPLAFPMALTINIRAETSAGASALSSFGQLGYTIACFGPLLTFGFIVDATGSFRT
 IFVLFAVATLTVIRGGYFATRQVYVEKLLNR

>RXN00193 TRANSLATE of: rxn00193.seq check: 1918 from: 1 to: 594
 KAFXQREGFISAFGFTVLVVIVSVITVNIFAFLLAWLLTRKLRGTNFFRTVFFMPNLLIG
 IVLGYTWTMINAVLSHYATTISADWKFGYAGLIMLLNWQLIGYMMIIYIAGLQNVPPPEL
 IEAAELDGVNKEWMLRHVTIPMVMSITICFLTLSNSFKLFDQNLALTNGAPGGQTEMV
 ALNIINTLFNRMNVEGVG

>RXN00378 TRANSLATE of: rxn00378.seq check: 9591 from: 1 to: 2610
 VDKAVNTAISDAKTAALKAGVGLNRATASEEEEDLSSSIKVSLAFELEGLSNAPSIMVVE
 KALEKIPGVSADLIYPSQTAWITATDRVHPETLIEVFEQFGIKAHLNSNSSLRRHQQLSA
 EVNREARLDYRSMRDAKRISPRVRRHNRQEMVHAVRARESGWIKRRNHTTSQHEDPMSG
 DVLFTRALITPKRLWVSLPFALIVLALSLSNPWFQFDYQWLSAVLAIPVVVWGAWPFHR
 AAAGGIRRGISALDATSSIAIAAAYAWSIAMLLFETPGGKSWSYPSWFAFDHGTLTQNE
 IYFDVACGITVLLLAGRLLTRRRSQSSLLAELGRQLIDPQRIVTVVRKHRLKRVVQELNI
 PVQEVVRNDDVKVPPNTTIPVDGTVIGGGSRIAASIIMGQDQRDVKVNDKVFAGSLNLES
 EIKVRVIRTGHRTRIAAVHRWVKEATLKENRHNRAAIRSAGNLVPITFTLAVVDFCLWAL

ISGNINAAFTTTTFLAVLACVAPVALALSAPLATRNSIEAAARHGILVRSGEIFRVLDDVDVT
AVFNVRVGTLTLDGEMTVETVTADKGEDPELVLRVAGALAMESHHAISKALVKASREARDTG
AGGEDVPHWIEVGNVEITEAGSFQATIELPLIKPSGEKIMRTTEALLWRPRSMTEVREHL
SPRLVAAATSGGAPLIVRWKGKDRGVITLSDHVRSDSSDAIAIEEQGIETMMLSRDTYP
VARRYADSLGITHVLAGIAPGKKAQVVRVAVHTRGSTVAMIGDESVMDCLVADVGVLGMV
DRPSDLRDDSDDPAADVVMREEVMSVPTLFLKLARRYAKLVNGNIALAWIYNGVAMVLAV
SGLLHPMAATVAMLASSLLIEWRSGRARKY

>RXN00412 TRANSLATE of: rxn00412.seq check: 7568 from: 1 to: 1080
VSHTASTPTPEEYSAQQPSTQGTRVEFRGITKVFSSNNKSAKTTALDNVTLTVEPGEVIGI
IGYSAGKSTLVRLINGLDSPTSGSLLNGTDIVGMPESKLRKLRNIGMIFQQFNLFQS
RTAAGNVEYPLEVAKMDKAARKARVQEMLEFVGLGDKGKNYPEQLSGGQKQRVGIARALA
TNPTLLLLADEATSALDPETTHEVLELLRKVNRELGITIVVITHEMEVVRSIADKVAVMES
GKVVEYGSVYEVFSNPQTQVAQKFVATALRNTPDQVESEDLLSHEGRLEFIDLTETSGFF
AATARAAEQGAFVNIVHGGVTTLQRQSFSGKMTVRLTGNTAAIEEFYQTLTKTTTIKEITR

>RXN00431 TRANSLATE of: rxn00431.seq check: 340 from: 1 to: 789
MVSIDTYNACVDFPIFDAKSRSMKKAFLGAAGGAIGRNQDNVNVVEALKNVNLHLREGDR
VGLVGHNGAGKSTLLRLLSGIYEPTRGSAIRGRVAPVFDLGVGMDFEISGYENIIIRGL
FLGQTRKQMKAKMEEIADFTTELGEYLSMPLRTYSTGMRIRLALGVVTSIEPEILLDEGI
GAVDAAFMAKARDRLQALVERSILVFASHSNDFLAQLCNTALWVDHGGQIREAGLVDPDV
EAYEGKGAGDHVRRLLTRMEEEE

>RXN00444 TRANSLATE of: rxn00444.seq check: 7535 from: 1 to: 837
MVLAQTKKARRSENHILPGWLLIPATLAMLLIIGPIFALLLQIPWDRSWELLTAPESLGT
ARLSIGTALFSTALCAIVGFPLALALHLYERSHPRVTSVLTVLVYAPLVLSPVVSGLALT
FLWGRRGFLGSWLDQVGLPIAFTTTAVVFAQVFVALPFFISTVTTALRGIPKQFEEIAAT
EGATRWEIMHKMIIPLAMPGIFTGMILGFARALGEYGATLTFAGNIAGVTRTIPLHIELG
LSSNDMDKALGAVIMLLAVVLIIGAIGALRLFSKVRKV

>RXN00466 TRANSLATE of: rxn00466.seq check: 8825 from: 1 to: 996
VQSRLSKILRSSVVGAVLALLAGCSNNADDDADSTSTGNSAFPVSIEHEFGTTTTIDDV
PERVVTLGVTDADIVLALGTVPGVNTGYKFFENGLGPWTDDELVEGKELTLLDSDSTPDLE
QVAALEPDLIIGVSAGFDDVVYEQLSDIAPVVARPAGTAAYAVAREEATNLVARAMGQSE
KGQELNEETDALIQAARDENPSFDGKTGTVILPYQGGYAYLPGDARGQFLDSLGLISLPE
AVLSRDTGDSFFVDVPAESVKDVGDDVLLVLSNDENLDITAENPLFETLNVVQKDAVIVA
TTEERGAITYNSVLSVPFALEHLAPRIAEALK

>RXN00523 TRANSLATE of: rxn00523.seq check: 9218 from: 1 to: 1026
MSLSHQLKRQRASRNSRRWLIVAALGVVTLGIFAFSLMWGEVIFYGPAQVLKVLSGQQVPG
ASYSVGVRLRLPRAVMGLTAGLAFGAAGVIFQTVLRNQLASPDIIIGISSGASAAGVICIVF
FGMSQSAVSAISLCASLAVALLIYLVAYRGGFSATRLILTIGIGIAAMLNSLVSYSLSKAD
SWDLPTATRWLTGSLNGATWDRAMPLIVTTVVLIPLLVANARNVDLMRLGNDASVGLGVA
TNRTRVIAIAAVALIAVATAACGPFAFVAFVSGPIAARILSGSGSLIIPSALIGGLIVL
IADLIGQYFLGTRYPVGVVTGAFGAPFLIYLLIRSNRAGVTL

>RXN00525 TRANSLATE of: rxn00525.seq check: 5915 from: 1 to: 1263
MSLAESILLALTSLRSNKMRALLTLLGVIIGIASVIGILTIGKALQDQTLNSLES LGAND
LSAQVEERPDEDSPEPDMFAFSGAANSSGNLIPEETVDTLRDRFAGSITGISVGGMGTOG
TLIGDTADLKSDLLGVNEDYMWNGVEMNYGRAITQDDVAAQRPVAVIAPDTFNTLFDAN
PNLALGSEVAFELNGQETFLRVIGVYKEAAAGGLVGSNPTVHTYTPYTVANDITHTEDGL
NTLSIRAAQGVDDQSLKGS LQTYFDALYANND SHHVAMLD FRKQIEEFNTILGAMSLGIS
AIGGISLLVGGIGVMNIMLVSVTERTREIGVRKALGARRRDIRLQFVVEAMIICFIGGIL
GVLLGGILGLIMSSAIGYISLPLSGIVIALVFSMAIGLFFGYYPANKAAKLDPIDALRY
E

>RXN00702 TRANSLATE of: rxn00702.seq check: 9529 from: 1 to: 1707
MSAPFSARTAWSTDPVLELESVAASYDDERTLAAPQISDVNLTLFEGEILLVVGRTGSG
KSTLLNAMSGAMPHATGGRLDGRVRVVGDRDRDFPPRMLSDVVGVVGQDPAASFITNTVE
EELAYSMEQLGLPPAVMRKRVEETDLLGIAELRYVPLAELSGGEQQRVAIGAVLTTRPA
LIILDEPTSALDPNGAEDVLATVTKLAHDLAMTVVLAEHRIERVLYQVDRVAHVAGDGHV

TVGTPEEIMADSDVAPPVELGRWAGWAPLPLSIRDARAHSAADMRRKRLYQRLVNVNKLHN
HAYQPLLIAEDIMVDFPEIRAVDGVNLSNLSGEITVLMGRNGCGKSSLLWALQSGSTRNQ
GSVQVLDEAAGFSWTDPKTLKPAKRRLVSMVVPQTPTDILYESTVHAELARSDKDAAPPA
GTTREILDSLVPNIPDHLHPRDLSEGQKLSLALSILQAAKPRVVFDEPTRGLDYDGKKS
LARSFQQLADDGHAILVVTHDVEFSALCADRVLFMASGKIISDGTAVEILPASPAYAPQV
AKITAGIQEESHWLTVSAVKAALGHGEIS

>RXN00726 TRANSLATE of: rxn00726.seq check: 2288 from: 1 to: 591
NAGRLYVDGDLIGYRERDGVLYEISEKDAKQRSDIGMVFNFNLFPHRTVIENIIEAPI
HVKKQPESKARARAMELLEQVGLAHKADAYPVQLSGGQQQRVAIARAVAMEPKMLMFDEP
TSALDPVELVGEVLRVMQLADDGMTMLVVTHEMGFAHEVADQVVFMAAGVVVEAGTPEQV
LDNPKEQRTKDFLSSLL

>RXN00732 TRANSLATE of: rxn00732.seq check: 6509 from: 1 to: 1647
NHLLLLPTVKADIIDNGVVTGDIGYIWHGTGGIMLALTLVQVACAIAGVYFGSKLSMRVGR
DLRSAIFGKVVNFSEMERMGQFGAPSLITRNTNDVQQVQMLVQMTSTLMISAPMLAIGGII
MAVRQDLGLSWLMVVSIPVLIIVVALIIVRMVPLFQTMQKRIDRINQIIREQLTGIRVIR
AFVREDVERERFTTASKDVADIGVRTGNLMALMFPAVMLIMNLSAVAVIWFGAQVESGE
TQIGTLFAFLQYIMQILMGVMAAFMFVMVPRAAVSADRIGEVLLETTPSVQAPETPAQPS
TSAGEIVFNATFAYPGADDPVLNNVSFRVAPGSTTATIGSTGSGKTTLIGLVPRLFDVT
EGDVTVDGTDVREPLKLVQKSLFSGTIANLRYGNEDATETQLWQALAI
QAADFVREMPEGLDSEIAQGGTNVSGGQRQLAIARALLKQPEIYIFDDSFSLADVSTDA
ALRRALSTNLPDATKLIVAQRVSTIRDADQIVVLDNGEVVGIGTHTNLLNTCGTYREIVE
SQETAQAQS

>RXN00759 TRANSLATE of: rxn00759.seq check: 3116 from: 1 to: 924
MLRYVGRRLQMIPIVFFGATLLIYALVFLMPGDPVQALGGDRGLTEAAAAEKIRQEYNLDK
PFIVQYLLYIKGIFVLDFGTTFSGQPVIDVMARAFPTIKLAIMALLFESILGIIFGVIA
GIRRGGIFDSTVLVLSLIVIAVPTFVIGFVLQFLVGKVGWLLPVTVGSNSTISALIMPAV
VLGAVSFAYVLRRLTRQSVSENLRADYVRTARAKGMSGFNVMNRHVLRLNSLIPVATFLGAD
LGALMGGAIVTEGIFGINGVGGLTYQAILKGEPTTVVSIVTVLVIVYIIANLLVDLIYAV
LDPRIRYA

>RXN00808 TRANSLATE of: rxn00808.seq check: 7354 from: 1 to: 1458
VLGTNVFGALAVMLFVRFLIPQPDASNFAEISYLPVAGFAYLAFIAIVAGMLVTFMFRP
VLDWQRPEDHHRNMVRNLVMRIPIYQAILCAVWVLIGIAIATLISASVSTSLALVVAFS
TLMAAAIVVLLTYLEAERLVRPVAASALARFEDSTLEPPVSQRLRMTWLLTLGIPVMGI
LLLIWGYSGIFGSDASGIMPAIALAFASLVGTGYNLRLVSSVVDPIRELQEAIRNRV
RGENDVQVDIYDGSEIGVLQAGFNEMMRGLRERQVRDLFGRYVGAEVAKRALEERPTLG
GEDRKVAVLFVDVIGSTTFVAVNHTPEEVVEALNEFFEHVVEVVRNKGVINKEFGDAALA
IFGAPLPLSDATGHALAAARELRAELKDLQLKAGIGVAAGHVAVAGHIGGHARFEYTVIGD
AVNQAAARLTEIAKTTTPGRTVTNASTLREANEAEQARWTLMKSVELRGRSQMTQIARPIRP
TLADRS

>RXN00828 TRANSLATE of: rxn00828.seq check: 8544 from: 1 to: 453
VRGGLNTPPHKWSADLAARIGTVFQDPEHQFVARTVRDELEIGPKIMKVDASERIEELL
DRLRLRHLENANPFTLSGGEKRRLSVATALVAAPKLLILDEPTFGQDPETFTELVTMLRE
LTDNGISIVSVTHDPDFIAALGDHHEVSAK

>RXN00832 TRANSLATE of: rxn00832.seq check: 2297 from: 1 to: 1050
MPFSWLKPIDYARIFVGVASIFIPLITLPSIIEALALIVAVILFCAFGVVKMAERLAHIL
GDPFGSLILTSIVIIEVILICAVMLGPADSTTAGRDSVMAVSMIIMGLVVGLCLLIGGL
RHGSMPHNGVGTPTYLVLIATFSVIAFAVPAFRGEYSTGQALVISTLTAVVYGFFLFRQM
GAQAGEFQEEVEAEKADDAKWEVPFRGLILITVLPVLLSHDMATVMDEVLASLGAPV
AMAGLIIATIVFLPETITSLKAAWTGEIQRVSNLAHGAQVSTVGLTIPAVLVIGVITGQD
VVLGETPINLLLLGTTIAVTAIAFSSKKVSAVHGSVLLMLFGVYMMSMFA

>RXN00934 TRANSLATE of: rxn00934.seq check: 9723 from: 1 to: 1083
VRIGMVCYPYSFDEPGGVQAHILDLARTFIAQGHEVQVLGPCSADTQVPDFVVRGGGSIPI
PYNGSVARLSFGPKMFKAVRTFLREGNFDVLHIHEPNSPSFSMAALRFAEGPIVATYHAS
SSGSKLLKAFLPVLSPMLEKVRAGIAVSEMARWQVEQVGGDPVLIPNGVETSMFKAARQ

IEPNDPVEIVFLGRRLDESRKGLDILLRALTRLDRPFTCTVIGGGTPREVAGINFGVRVSD
 EEKAAAILGRADIYVAPNTGGESFGIVLVEAMAAGCAVVASDLEAFSLVTDSEAAQPAQVL
 FKTGSDADLAKKLQALIDDPSSRSTLIAAGLKRANAYDWSTVSTQVMAYETIAIDKVRLL
 G

>RXN00939 TRANSLATE of: rxn00939.seq check: 3908 from: 1 to: 1236
 MTRQKTQPFLEKFSKYYPGVMIAALAVGLITLNLVELALTLVVIACPGALVISIPVSIVA
 GIGRSKADGVLIKGEYLETSKAVDTVVVDKTGTLTNGRPELTNVDVLDPAYSDDEVLTLL
 AARAETASEHPLAEAIIRGAENRGLTVAMVEKAEPVAGRGIRADVDGATVAVGSADLLDH
 TPDNTRILELNEQGRITAMYVGINGKAVGIVAVADTIRDDAPAAIRSLHNKGIRVVMATGD
 AERVARNVAAELGVDEVRAELMPEDKLEIVKELQAQGRVVAMVGDGVNDTPALATADIGV
 AMGAAGSPAAIETADIALMADKLPRLPYALGLAQRTVTRMRVNIGIALLTVTILLAGVLL
 GGVMTSIGMLVHEASVLLVIAIAMLLLRPTLTKEDKDKADVSTADAAKETLSA

>RXN00960 TRANSLATE of: rxn00960.seq check: 4118 from: 1 to: 1035
 MARHCCSNRYASTVFSGLIAYGASQALYPWLLKDHQSVTEIDLDAGALQPYFNIEMPPPF
 EVMTALLLAFCLGLGMAVIKSDTLFKVTRELERVVMKTITAFVIPLELPLFIIFGIFLGMGM
 NGGLLEIMSAFGKVLILAVVGTLLFLAIQFIIAGAVSKKNPWKLFKNMLPAYFTALGTSS
 SAATIPVTYQQTLKNDVDVNVAGFVVPLCATIHLGASMMKIGLFTFAVVFMYDMEVGVGL
 SIGFLMLGITMIAAPGVPGGAIMAATGMLASMLGFNTEQVALMIAAYIAIDSFGTAANV
 TGDGAIAIVNVKFAKGQLHTTSPDEIEEDDRVAFDITPSDVEHHK

>RXN00980 TRANSLATE of: rxn00980.seq check: 2367 from: 1 to: 1794
 MLADAFMIAAAIVAGWPQASAYQALRIRMVSIIDLLVVVAAVAGAMFINNYWESAAVTFLF
 ALGKALERATMNRTRKALSDLVDAAPETATRLNADDSTEVVELWELEPGDIVLVRNGEQI
 PVDGNVIAGVGGIDESNITGESMPAEKQGSDVYAGTWLRSGVLRVEATGIGSDSTLAKI
 IHRVEDAQDDKARTQTFLEKFSKYTPGVMIAAAVVGLITWDELALTLVIGCPGALVI
 SIPVSIVAGIGRAARDGVLIKGEYLETAAKVDVVVDKTGTLTTRPELTDVEVIEPAY
 SQGEVLELAARAETASEHPLADAIIRGAQDRGLSTTLVEAAENITGRGIIANVDGQAVAV
 GSAELLDHEPDSTRIELNAEGKTAMFVGVNNGHAIGIVAVADAVRSDSASAIESLHKAGI
 QVVMATGDAHRVAQNVASKLGVDEVYSELLPEQKLELVRDLQAAGKTVAMVGDGVNDTPA
 LAAADIGVAMGVAGSPAAIETADIALMADRLPRLAHAVTLAKRTVTRMRINILIALATVM
 VLLAGVLFGGVTMSVGMLVHEASVLLVISIAMLLLRPTLKDAAQASDIKRSEIQQIA

>RXN01000 TRANSLATE of: rxn01000.seq check: 4854 from: 1 to: 846
 MSTLTSHRTVPAPSSPPARPKNLARNIVAIVAALIVLIATGTLKIEWNELPQMPAQVWHY
 LELMFSDPDWSKFGRAVQEMWRSIAMAWLGAILCVVSVPLGMLAARGVGPYWLRTVLRF
 VFAVIRAFPEVVIAIILLTVTGLTPFTGALALGISGIGQQAQWYEAIESTPTGPSEAVR
 AAGGTTPEVLRWALWPQVAPSIASFALYRFEINIRTSAVLGIVGAGGIGSMLANYTNYRQ
 WDTVGMILLIVVVVATMIVDLISGTIRRRIMKGASDRVVAPSN

>RXN01002 TRANSLATE of: rxn01002.seq check: 1757 from: 1 to: 804
 MNSDASATTNSWAINFDHVSVTYPNGTKALDDVSLTINPGEMVAIVGLSGSGKSTLIRTI
 NGLVRATEGTVTVGPHQINTLKGKALRDARGQIGMIFQGFNLSSRSVFQNVLVGRFAHT
 AWWRNLLGFPTHEHDQIAFAHALESVGILHKVWTRAGALSGGQKQRVAIARALSQDPSVML
 ADEPVASLDPTTAHSVMRDLENINNVEGLTVLVNLHLIDLARQYTTTLVGLRAGKLVDG
 PISEATDKDFEAIYGRPIQAKDLLGDRA

>RXN01141 TRANSLATE of: rxn01141.seq check: 9956 from: 1 to: 825
 LSTALAGAARYVTSTSNNEPADNTPLTIGYVPIAGSAPIAIADALGLFKKHGVNVTLLKKY
 SGWSDLWTAYATEQLDVAHMLSPMTVAINAGVTNASRPTLSFTQNTNGQAITLASKHYG
 SVNSAADLKGMLVGIPFEYSVHALLLRDYLVSNVAVDPIADLELRLLRPADMVAQLTVEGI
 DGFIGPGPFNERAISNGSGRIWLLTKQLWDKHPCCAVAMAKEWKAEHPTAAQGVNLALAE
 ASAILSNPAQFDSSARTLSQEKYLNQPATLLDGPS

>RXN01142 TRANSLATE of: rxn01142.seq check: 3960 from: 1 to: 498
 LTARGNIDFGLRSARPSLSKTERADITRTHLEQVGLTDAAERRPARLSGGMQQRVGIARA
 FAIDPPIMLLDEPFGALDALTRRELQQLLNIWEASRRTVVMVTHDVDEAILLSDRVLM
 SKSPEATIITDIPVNLPRPRHELSSEDASVEAETTALRKRMHLHLEH

>RXN01164 TRANSLATE of: rxn01164.seq check: 868 from: 1 to: 1635

VTLEFVRLALAAVGGLEFVFASNEPIGWFWAGIVGTALFFISLAPWDLGVPOKRRKKNEPVP
 FLOQMSTGPTVVQGMLLGFVHGLVLYLQLLPWIGEFVGSLLPYVALSVVEALYSIALGAFG
 VLIARWRDVKVLLFPAMYVAVEYLRSSWPFDFGFAWVRLAWGQINGPLANLALGGVAFVT
 FSTVLAAVGVAMVLIISKKRLAGAIITASVIAIGAVSSLYVDRNGTSDESIEVAAIQGNVP
 RMGLDFNAQRRAVLANHARETLKLDEQVDLVIWPENSSDVNPFSDAQARAIIDGAVEHVQ
 APILVGTITVDEVGPRNTMQVFDPEGAEEYHNKKFLQPFGEYMPFREFLRIFSPYVDSA
 GNFQPGDGTGVVEMNAANLGRAVTVGVMTCYEVIFDRAGRDAIANGAEFLTTPTNATFG
 FTDMTYQQLAMSRMRAIEFDRAVVVAATSGVSAIVNPDGSIQNTRIFEAATLTESIPLK
 DTVTIAARVGFYVELLLVIIGVLAGLFAIRMNSRSKSAKGSARPAQVRVKKVPAKKAATN
 RRKVK

>RXN01168 TRANSLATE of: rxn01168.seq check: 6703 from: 1 to: 810
 MSSEAVDATTLVLIPTYNELENLPLIVDRVRTATPDVHVLIVDDNSPDGTGERADKLAAD
 DDHIFVLHREGKGGGLCAEYMAGFQWGLERDYQVLCEMDADGSHAPEQLHLLLAIEITNGAD
 LVIGSRYVPGGRVNWPKNRWLLSKGGNVYISVALGAGLTDMTAGYRAFRREVLEALPLD
 ELSNAGYIFQVEIAYRAVEAGFDVREVPITFTEREIGESKLDGSFVKDSLLEVTKWGLKH
 RGGQAKELSKEMVGLLNYEWHFKKRNTWL

>RXN01285 TRANSLATE of: rxn01285.seq check: 1049 from: 1 to: 726
 LNVITPDNTFTAIIGPNGCGKSTLLRGFSRVLNPHQHGKVLDDGRQLDSFKPKIEIARELGL
 LPQTSIAPEGIRVYDLIARGRAPYQSLIQQWRTSDEDAVAQALASTNLTELAARLVDELS
 GGQRQRVVWVAMLLAQQTPIMLLDEPTTFLDIAHQYELLELLRAFNEAGKTVVTVLHDLNQ
 AARYADHLIVMKDGHVHATGTPEEVLTAEMVQGVFGLPCIISPDPVTGTPTVVPLSRRA
 GA

>RXN01298 TRANSLATE of: rxn01298.seq check: 8940 from: 1 to: 930
 VSTLISEPEVDKLRKRAKRSRTEWWLAAALLAPNLLLLAIFTYRPLLDNFRLSFFWNWI
 SSPTSTFIGFDNYVEFFTRSDTLQVVLNTVIFTACAVIGSMVLGLLLAMLLDQKLFGRNF
 VRSMVFAPFVISGAAIGVAFQFVFDPNFGLVQDLLGRIGVDSPOFYQNPWALFMVTFTF
 VWKNLGYSFVIYLAALQGLNKDLSEAPVDGASAWTRFWKVTLPLQLRPTTFELSIPTVLN
 SVQVFDIIHTMTRGGPLGNGTTTLVYQVYTETFTNYRAGYGATITILFLLLLIITVIQV
 RYMDKENKQK

>RXN01323 TRANSLATE of: rxn01323.seq check: 658 from: 1 to: 2265
 MAQTPAKIPAAALNFIDVDLGVGTGMTCTSCSARVERKLNKLDGVEATVNYATESAQVSYDP
 SKVSPEQLIKTVEDTGYGAFTMASAAAESEEDNAPADSGQSRIDAARDHEAADLKHVRIV
 SALLSVPVVLVSMIPALQFNWQWAVLTLVTPIFFWGGSPFHKATWANLKRGSFTMNTLV
 SLGTSAADLWLSLWALFIENAGHPGMMEMHLLPSASTMDEIYLETVAVVITFLLLGRWFE
 TKAKGQSEALRKLLDMGAKDAVVLRDGAEVVPVNLKLGDFVITRPGEKIATDGEVDE
 GSSAVDESMLTGESIPVEVTKGSKVTGATLNTSGRLMVKVTRIGADTTLSQMAKLVTDAQ
 SKKAPVQRLVDQISQVFVPVIVIAIATLIAHLVFTDAGLAPAFTAATAVAVLIIACPCALG
 LATPTALLVGTGRGAQLGLLIKGPETESTKKVDTIVLDKTGTVTGTMSVTDVTAINYS
 ETEILEFAAAVESASEHPAQAIAKAAEHEQVTDQNTAGQEVTVGVVGRGHEVRVGRPSST
 LIDALLHPFQHAQKIGGTPVVVTIDGVDSGIITVRDVTVKDTSAAEIRGLKELGLTPILLT
 GDNEGAAKSVAEEVGIDQVIANVLPHEKVQNVLEALQAQGNVAMVGDGVNDAAALAQADL
 GLAMGAGTDVAIEASDITLMNNDLRSVDAIRLSRKTTLGTIKGNLFWAFAYNVALIPVAA
 IGLLNPMLAGIAMAFSSVFVVSNSLRRLRGFKARSN

>RXN01338 TRANSLATE of: rxn01338.seq check: 9102 from: 1 to: 1902
 KTYTPNPWMLFIRSFDDGIITVAALVAIAIHLILWLALDLGLAKNWPLIAIVIVGGIPLM
 WDLVLSAIKTRGGADTLAAVSIITSVLLGEWLVAIIIVLMLSGGEALEEASRRASGTLT
 ALARRAPSTAHRLLGATILDGTEEIAVEEITVGDVAVLPHELCPVDGEIVAGHGTMDES
 YLTGEPYVVSXSKGSQAMSGAVNGDTPLTIVATKLAHDSRYAQIVGVLHEAENNRPEMRR
 MADRLGAWYTVIALALGGLGWIVSGDPVRFLAVVVVATPCPLLIAPVVAIIGAISLAARR
 GIIIVKNPGLMENASGVKTMFDTGTLTGRPVITDIHTAPGVEEDTVLALAASVERYSR
 HPLADAIREGAKRELHLPDVVEVSESRPGQGLTGTVGEHLVRITNRRSTLEIDPDSKNYI
 PVTSSGMESVVLVDKYAALIRLRDEPRASASEFIAHLPPKKHKVDKLMIIISGDRASEVRY
 LADKVGIDEVHAEASPEDKLNIVNRHNEHGATMFLGDGINDAPAMAVATVGVAMGADSDV
 TSEAADAVILDSSLERLDDLLHISARMRRIALQSAGGGMALSVIGMILAVFGFLTPLMGA
 IFQEVIDVLAILNSARVALPRGAISDFDTQEKVS

>RXN01411 TRANSLATE of: rxn01411.seq check: 3735 from: 1 to: 765
 MLGVGWRIPFLMAVPLGLIGWWIRTGAQENVRPASERPEAPIKQALRTEWKMMMLRVGGFI
 SCTGLSFYIFTTYMTTFLRSTVGLGTLVLAGNIIALSMAAIVAPFVGRAIDKFPRRNIM
 AFATLSTVIMAI PAYIIAGQGTLTASLIAQVMLGIGAVTANCVTSVMMAEVFQEVTRGTS
 AGITYNVTYAIFGGSAPFISTALVSWTGSPLAPAVYMIIALFAFTASRFIPETSPVFVT
 ATPAIKAPKVLVNP

>RXN01808 TRANSLATE of: rxn01808.seq check: 4151 from: 1 to: 1149
 QSLACKELAWMRGGAPARTSKPGFRLEAAEALIAEVPAPRDKVELMAFSKSRQGRVIEL
 EDATVATPDDRILVEDLTWRLAPGERIGLVGVNGSGKTTLLRTLAGEQPLQAGKRIEGQT
 VKLGWLRQELDDLDLSRRLIDCEDVASVMMGDKQVSASQLAERLGFSPKRQRTFPVGD
 SGGERRRLQLTRVLMAPENVLLLDDEPTNDLDIDTLQELSLLDGWPMTMVVISHDRYLIE
 RVTDSWALFQDGLTNLPGGIEEYLQRRAMAAAEDSGVLNLGAATQAGTFSATEQAA
 TSVESSGISSQERHRTKEMNALERKMGLDQQMDKLNQQLADAAEAMDTIKLTELDTKL
 RAVQEEHGELEMQLWLELGEIEG

>RXN01939 TRANSLATE of: rxn01939.seq check: 574 from: 1 to: 1731
 MTTNIPQTPNHEGEQPLLELKDLKISFTSSTGVVDVARGANLTIYPGQSVIAIVGESGSGK
 STTAMSIIGLLPGTGKVTESIMFDGQDITGLSNKQMEKYRGSEIGLVPODPMNTLNPVW
 RIGTQVKESLRANHVVPVPGSEMDKRVAEVLAEAGLPDAERRAKQYPHEFSGGMRQALIAI
 GLAARPKLLIADPTSLDVTQVRQILDHLETITKDLGTAVLFI THDLGLAERAHLV
 MHRGRIVESGPSLKILRNPHYPYTQRLVKAAPSLASARIQSAEQGIESAELLSATAVAE
 GTIPEMEEKVIEVKNLTREFDIRGARGDKKKLKAVDVVSFFVRKGT TALVGESGSGKST
 VANMVLNLLIPTSGEVLYNGTDLTSLSHKEIFQMRRLQVVFQNPYGS LDPMYSIYRCIE
 EPLTIHKVGGDRKAREARVAELLDVSMRSTMRYPNELSGGQRQRIAIARALALNPEV
 IVLDEAVSALDVLVQNLITLLAELQQLKLTLYLFI THDLAVVRQTADDVVMQKGRIVE
 KGRTDDIFNDPQQHYTRDLINAVPGLGIELGTGENLV

>RXN01995 TRANSLATE of: rxn01995.seq check: 3763 from: 1 to: 1338
 MDIRQTINDTAMSRQWFIVFIAVLLNALDGFVLAAMSFTANAVTEEFGLSGSQLGVLLS
 SALFGMTAGSLLFGPIGDRFGRKNALMIALLFNVVGLVLSATAQSAGQLGVWRLITGIGI
 GGILACITVVISSEFNNKNGMAMSIYAAGYGIGASLGGFGAAQLIPTFGWRSVFAAGAI
 ATGIATATFFFFLPESVDWLSTRPAGARDKINYIARRLGKVGTFELPGEQSLSTKKAGL
 QSYAVLVNKENRGTSIKLWVAFGIVMFGFYFANTWTPKLLVETGMSEQQGIIGGLMLSMG
 GAFGSLLYGFLTTFKSSRNTLMTFMVLSGLTLILFISSTSVPSTAFASGVVVGMLINGCV
 AGLYTLSPQLYSAEVRTTGVGAAIGMRVGAISAPLLVGGLLDGWSPTQLYGVAVIVI
 AGATALIGMRTQAVAVEKQPEALATK

>RXN02062 TRANSLATE of: rxn02062.seq check: 5414 from: 1 to: 1170
 MRVGMMTREYPPPEVYGAGVHVTELTRFMREIAEVDVHCMGAPRDMEGVFVHGVDPALES
 ANPAIKTLSTGLRMAEAANNVDVHSHSTWYAGLGHLAARLHGIPHVATAHSLEPDRPWK
 REQLGGGYDVSSWSEKNAMEYADAVIAVSARMKDSILAAYPRIEPDNVRVVLNGIDTELW
 QPRPTFDDAEDSVLRSLGVDPQRPIVAFVGRITRQKGVHEHLIKAAALFDESQVLVLCAGA
 PDTPEIAARTTALVEELQAKREGIFWVQDMLGKDKIQEILTAADTFVCPSTIYEPLGIVNL
 EAMACNTAVVASDVGGIPEVVVDGTTGALVHYDENDVETFERDIAEAVNKMVADRETAAK
 FGLAGRERAINDFSWATIAQQTIDVYKSLM

>RXN02096 TRANSLATE of: rxn02096.seq check: 3261 from: 1 to: 1692
 MGLDVSDEQIEHAARLAQAHD FIDRLPNKYEEVIGERGLTSLGGQRQRIALARAFLAHPK
 VLVLD DATSAIDASTEDRIFQALREELHDVTILIIAHRHSTLELGDRVGLVEDGRVTALG
 PLSEMRDHARFSHLMALDFQDSDHPEFTLDNGSLPSQEQLWPEVSTEKQYKILAPAPGRG
 RGMSMPATPELLAQIEALPAATEETRV DAGRLRTSTSGFKLLSLFKQVRWL VVAVIALLL
 VGVAADLAFPTLMRAAIDNGVQAQSTSTLWWIAIAGSVVVLWSWAAAAINTIITARTGER
 LLYGLRLRSFVHLLRLSMSYFERTMSGRIMTRMTTIDIDNLSSFLQSGLAQT VVS VGTIG
 VVTMLAITDAQLALVALSVVPIIIVLTILIFRRISSRLYTASREQASQVNAV FHESIAGLR
 TAQMHRMEDQVFDNYAGEAEFRRLRVKSQTAIAIYFPLGALSEIAQALVLGFGALQVT
 RGDISTGVLVAFVLYMGLMFGPIQQLSQIFDSYQQAAGVFRRITELLATQPSVQIWAPTG
 TLGRLPRSLYCLTTSPSAIQTIRS

>RXN02348 TRANSLATE of: rxn02348.seq check: 8038 from: 1 to: 1884
 MLNRMKSARPKSVAPKSGQALLTLGALGVVFGDIGTSPLYSLHTAFSMQHKNKVEVTQENV

YGIISMVLWTITLIVTVKYVMLVTRADNQGQGGILALVALLKNRGHWGKFVAVAGMLGAA
LFYGDVVITPAISVLSATEGLTVISPSFERFILPVSLAVLIAIFAIQPLGTEKVGKAFGP
IMLLWFVTLAAGLIPQIIGHPEILQSLSPHWALRLIVAEPFQAFVLLGAVVLTVTGAEL
YADMGHFGARPIRVAFWFCVMPALILTYLGQALVINQPEAVRNPMFYLAPEGLRIPLVI
LATIATVIASQAVISGAYSLTKQAVNLKLLPRMVIRHTSRKEEGQIYMPLVNGLLFVSVM
VVVLVFRSSESLASAYGLAVTGTLLVSVLYLIYVHTTWWKTALFIVLIGIPEVLLFASN
TTKIHDGGWLPPLIAAVLIVVMRTWEWGS DRVNQERAELELPMDKFLEKLDQPHNIGLRK
VAEVAVFPHGTSDTVPLSLVRCVKDLKLLYREIVIVRIVQEHVPHVPPEERAEMEVLHHA
PIRVVRVDLHLGYFDEQNLPEHLHAIDPTWDNATYFLSALTLSRLPGKIAGWRDRLYLS
MERNQASRTESFKLQPSKTITVGTTELHL

>RXN02354 TRANSLATE of: rxn02354.seq check: 8723 from: 1 to: 834
MTKRTKGLILNYAGVVFILFWGLAPFYWMVITALRDSKHTFDTFPWPTHVTLDNFRDALA
TDKGNFLAAIGNSLVISVTTTIAIVLVGVFTAYALARLEFPKGKIVTGIIAASMFPGI
ALVTPFLQLEFGDLNWIGTYQALIIPNISFALPLTIYTLVSFFRQLPWELEESARVDGATR
GQAFRMILLPLAAPALFTTAILAFIATWNEFMLARQLSNTSTEPVTVAIARFTGPSSFEY
PYASVMAAGALVTIPLIIMVLIFQRRIVSGLTAGGVKA

>RXN02356 TRANSLATE of: rxn02356.seq check: 7192 from: 1 to: 996
MATVTFDKVTIRYPGAERATVHELDLDIADGEFLVLVGPSCGKSTTLRALAGLEGVESG
VILDKGDTVGTQEPADRDIA MVFQNYALYPHMTVAKNMGFALKLAKLPQAQIDAKVNEAA
EILGLTEFLDRKPKDLSGGQRQVRAMGRALVRDPKVFLMDEPLSNLDAKLRVQTRAEVAA
LQRRLGTTTVYVTHDQVEAMTMGDRVAVLKDGLLQQVAPPRELYDAPVNEFVAGFIGSPS
MNLFPANGHKMGVRPEKMLVNETPEGFTSIDAVVDIVEELGSESYVYATWEGHRLVARWV
EGPVPAPGTFVTFESYDAAQAHFDESGERIA

>RXN02391 TRANSLATE of: rxn02391.seq check: 7541 from: 1 to: 399
MTQSDLPDDVQELVTKIFGLARDGGAESAATLGAYVDNGVDVNLNSQDGNTLLMLAAYAG
HADVVQALIERGADVDRVNNRNQTPLAGAI FKKEEAVIEALLAGGADPYAGTPTAVDTAK
MFGREDLVARFES

>RXN02442 TRANSLATE of: rxn02442.seq check: 5164 from: 1 to: 849
MKFFTDALIVPFDVSFISRALVAGCLAAILCSLIGTWVILRRLTFFGDAMSHGLLPGVAT
ASLLGGNLMFGAAISALIMSAGVVWTSRKSSLSQDVSIGLQFITMLSLGVVIVSHSDSHA
VDLTSFLEFGDILGVRPSDIFI IAIATVLGGLTIFLFHRQFTALAFDERKAHTLGLNPRFA
HLLMLALIALATVVSFQVVGTTLLVFGLLIGPPATAALLVQDKASISLIMIVASLLGCAEI
YLGLLISWHASTAAGATITLLSAAIFFATLLTKSAISRLNFTA

>RXN02447 TRANSLATE of: rxn02447.seq check: 8454 from: 1 to: 1095
TVVPVYLAELAPLEIRGSLTGRNELAIVTGQLLAFVINALIAVTLHGVIDGIWRIMFAVC
ALPAVALFLGMLRMPESPRWLVNQGRYDDARRVMETVRTPERAKAEMDEIIAVHSENNAA
LPGVKQSSGQASGVSSKHTHMSIGEVLSNKWLVRLLIAGIGVAVAQQLTGINAIMYYGT
RVLEESGMSAEMAVVANIAFGAVAVIGGLIALRNMDRDRRTTFIIGLSLTTFHLLIAA
AGTLLPEGNSIRPFAIMILVVGFLSMQTFNLVAVVWVLAEIFPVRMKGIGTGISVFCGW
GINGVLALFFPALVSGVGITFSFLIFAVVGVI ALAFVTKFVPETRGRSLEELDHAFTGQ
IFKKA

>RXN02455 TRANSLATE of: rxn02455.seq check: 2559 from: 1 to: 1269
LKRLTRIASISMASMLAAASLVACSGSTDEEGDVYFLNFKPEQDVAYQEIAKAYTEETGV
KVKVVTAASGSYEQTLKAEIGKDEAPTLFQVNGPAGFITWQDYMADMSDTEVAKQLTDDI
PPLTTEDGEVRGVFPFAVEGFGI IYNDEIFDKYIATSGAKIKSTDEITSYQKLKEVAEDMQ
AKKDELGIEGAFASSTLSSEDWRWQTHLANAPIWQEYQDKGVEDTNEIEFSYNKEYKNL
FDLYLENSTVEKSLAPSKTVSDSMAEFAQGKAAMVQNGNNAWSQISETSGNVVKEDKIKF
LPMYMGLPDEEKHGINVG TENYLVGNSEASEVDQATKDFVDWLFTSEAGKEHVVKDLGF
IAPFESYTAENTPNDPLSEQVAEAIANKDLTTYPNWFQYFSPSQQFKDDFGQDLSQYASGK
LKW

>RXN02515 TRANSLATE of: rxn02515.seq check: 4857 from: 1 to: 756
MSTLEIRNLHAQVLPSDESAEPKEILKGVNLTINSGEIHAIMGPNGSGKSTLAYTLGGHP
RYEVTAGEVLLDGENILEMEVDERARAGLFLAMQYPTIIPGVSVANFLRSAATAIRGEAP
KLREWVKEVRTAQEALAI DPEFSNRSVNEGFSGGEKKRHEVLQLDLLKPKFAIMDETDSG

LDVDALRIVSEGINSYKQETEGGILMITHYKRILNYVKPDFIHVFANGQIVTTGGAELAD
KLEADGYDQFIK

>RXN02549 TRANSLATE of: rxn02549.seq check: 8075 from: 1 to: 2703
MVHAKQTKKPLPRFLHSAHFYVWIVLGFVVFQAQPYGQVAADTKLDLLLNPAAGFLTALHA
WTDFTTLGQLQONQAYGYLFPQGFFFLITDFLPDWIAQRLWWVLVLGLGFSGFYALVARLG
IGNPAFRVIAALLFALSPTTLTTLTAISSETWPIMLAPWVCLPLLSRNVDARAIALSLLP
AACMGAVNATATMAALI PAALILLYRGLFLRLLLLWGMGVLAVNSWWIGPLLLVLGKYAPPF
TEFIESSSVTTSWLNVPVEILRGTTSWTPFVDTERQAGYLLVNDALFVTL SVLVAALGLIG
LTLMKHRGLWAFMLAIGLLILGSAHLTAVQEFLDGPGAALRNHFKFDLLVRMPLMVGVAA
LGSHISLPLLGTTALTSGQGKHHTIPLPLQKRQAAGLLVVI IAVGALAPAWSARLLPQGT
WDEVPDYWYEATEFLNQATGTRTLIWSPSPFARQDWGWRDEPAQPLLDVWPWAVRDAIP
LVPPEAIRGLDGLDDLGTGLTGLNDEALKRLGIGAVLVRHDLEADPDIEVDLPGEKHTFG
SQGQVDVYLTDPDRNMWITSGTSKQLPTVAGGGEILSLLDTINGYSPRTLVSENAQIVTD
TPQLVGTYNGDGTSSAALASLDETEVKNRIVDYPASAGPMTQVVQEGSITASSSGSDATSF
GGADPDRSLNSLLDHRNTAWYPTPGDTSPWLEVSGTGTTLSISPRSTVTATITSGDSVM
VREFEKGRTTTTVTLAEPEARIEFDGFGVISELSLEGLSRTITVPETSPDVQQFVFQRLTV
PTSFLDRTFTVPRHMSVTVEAQSCVTLLELDGDRIDCGPSNSPPEPTRCAPNRNGSPSPNP
LRSPLESQQQTSRQHPPTACSSPRALSIQVPARLSTPPPPFQSNSTPPPKVSSSPRTPPA
S

>RXN02570 TRANSLATE of: rxn02570.seq check: 2673 from: 1 to: 642
MNPLTWIIGAFSMWIVVLGVNKLGLSIAVIIIAQVVMIRVRNVSVLASTALLSVPALAS
MALIHMPYSSDGWLIALTLTARFSALMSIFLLAATAITIPELVKSLYRWPKLAYIVGSAL
QMIPQGGKQTLALVRDANALGRSVKGPVRAVKYVGLPLITHLLSAGAARAIPLEVAGLDR
PGPRTVLVEVVEGRVEKHCRWLLPLLAVGMAWWL

>RXN02595 TRANSLATE of: rxn02595.seq check: 5016 from: 1 to: 1164
VIVVAMASIMACLKAAARLNNPMKILLLCWRDTHHPQGGGSERYLERVGEFLADQGHEVVF
RTAGHTDAPRRSFRDGVRYSRSGGKFSVYPKAWVAMMLGRVGIGTFSKVDVVVDTONGIP
FFGKFFSGKPTVLLTHHCHKEQWPVVGRLAKVGWLIIESQIAPRAYKTAPYVTVSEPSAE
ELIALGVDDQRIHIVRNGVDPVPLHTPKLDRDQGHAHTLSRLVPHKQIEHAMDVVAALDG
VVLDDVESGWWQKELVDYARTLGVS DRVVFHGGQVAEDHKHALLERATIHLMPSRKEGWGL
AVTEAAQHGVPTIGYRSSGGLRDSVVDGETGLLVDSKAELISATKTLIDASLRSKLGAS
AKQRAENYKWDTAGAQFEELLLGLASKK

>RXN02614 TRANSLATE of: rxn02614.seq check: 5216 from: 1 to: 729
MTATLSLKPAATVRGLRKS YGTKEVLQIDLTINCGEVTALIGRSGSGKSTILRVLAGLS
KEHSGSVEISGNPAVAFQEPRLLPWKTVDNVTFGLNRTDISWSEAQERASALLAEVKLP
DSDAAWPLTSLGGQAQRVSLARALISEPELLLLDEPFALDALTRLTAQDLLLLKTVNTRN
LGVLLVTHDVSEAIADHVLDDGAIHSLTVDIPGDRRTHPSFASYTAQLLEWLEIT
TPA

>RXN02795 TRANSLATE of: rxn02795.seq check: 7318 from: 1 to: 1437
VLKVS DLTVGNNFVHNVSFEVNPGERVGIIGESGSGKSLTALSIMGLTDLP TTGQITFNG
KPSATFRGTRIAMVVFQEPMSALNPLMRIGRQIEEMMTLHGASKKDARARLKSLLIDVSLP
ERTASAYPHELSSGGQRQALIAMALANDPDLICDEPTTALDVVVQKQIVDLLLLRLTKER
GTALLFITHDLGLIARTCERLLVMKSGETVERGDTEAILRSPAHSYTOQLLDASILDQPE
IASDSGAPVVIDVEEASKSFKETTALHKVSLAVRKGDLLGIVGGSGSGKTTLKLIAGLD
KPTTGTVAVTGGVQMVVFQDPQSSLNPRMKIKDIVAEPLLGWNAAEKTTRVAEVITQVGLS
PDVLD RYPHEFSGGQRQRIS IARALAIKPAILLADEPVSALDVSVRKQVLDLLQQLVEEY
GITLVFVSHDLAVVRHLCTTVWVMEQGRVLEQGPIDSVYDHPQTEYTKELLDAVPRLSL

>RXN02925 TRANSLATE of: rxn02925.seq check: 5237 from: 1 to: 2217
MSTPHHHGDHPAPETDHTHHHPNHAGHEHHADAATHGQAMPDHDPHSTVDEEHQVHSHGEH
AGHSAAMFRDRFWWSLILSVPVVFFSPMFADLLGYNIPEIPGAYWIPPVLGTIIFLYGGT
PFLKGAMTELKSRQPGMMLLIAMAITVAFIASWVTTLGLGGFHLDFWWELALLVTIMLLG
HWLEMALGAASSALDALAALLPDEAEKVVDGTTTRTV AIS ELAVDDVVLVRAGARVPADG
TIIDGAAEFDEAMITGESRPVYRDTGETVVAGTVATDNTVRI RVEATGGDTALAGIQRMV
ADAQASSSRAQALADRAAALLFWFALITALITAVVWTIIGSPDDAVVRAVTVLI IACPHA
LGLAIPLVIAISSERAASKSVLIKDRMALEHMRTIDVVLFDKTGTLTEGAHAVTGVPAT

GIAEGELLALAAAAEADSEHPVARAIVTAAAAHPEASQRQLRATGFTAASGRGIRATVDG
 AEILVGGPNMLREFNLTPGELADITGSWAQRGAGVLHVVRDGEIIGAVAVEDKIRPESR
 AAVRALQARGVKVAMITGDATQVAQAVGKDLGIDEVFAEVLPPQDKDTKVTQLQERGLSVA
 MVGDGVNDAPALARAEGVIAIGAGTDVAMESAGVVLASDDPRAVLSMIELSHASYRKMVQ
 NLVWATGYNIVAVPLAAGVLAPIGVLLPPAAAAAILMSLSTIIVALNAQLLRRIDLDPAHL
 APTDGKEEKAHVSSAAPVR

>RXN02933 TRANSLATE of: rxn02933.seq check: 4913 from: 1 to: 810
 MPLSGKIGGFIVAVFVLAALSFIWTFDPVQAFPPQERLEGSSLRHLLGTDTRYGRDVLSSQ
 IMVGSRVTLVLVGIIAIAIAALIGTPLGIAAGMRGMVETFFVMRGADLMLAFPALLLAIS
 GAVFGASTWSAMVAIGIAGIPSFARVARAGTLQVTSQDFIAAARLSKVSSARIALRHILP
 NITSMLIVQASVAFALAILAEALSFLGLGTTTPDPSPWGRMLQTAQASIGVTPMLAVWPG
 AAIALTVLGFENLFGDGLRDAIDPKREVGRA

>RXN02945 TRANSLATE of: rxn02945.seq check: 2147 from: 1 to: 933
 MTTALGTRVVARNFGRHASRENPAKLDINFEIAPGERILLTGASGAGKSTLLAALAGVL
 GGSDEGVSTGELLVDAPSIGLVLPQDPDSQVIASRIGDDVAFGCENLQIPREEIWPRVERA
 LELVGLDLPLSHPTKYLSSGGQKQRLALAGVIAMGARLILLDEPTANLDPQGGQKNVVAVD
 RVVQETGATLIVVEHRHELWVNIIDRIISITDGEDVQPAELIKVGQLPGAQPSTSKPILW
 ANDLLCTWGGRLRSFEVPEGASTVITGPNAGKSTLALTMGGLLPRKVGSWNSLTRCAAL
 TRPRTSGVQLI

>RXN02975 TRANSLATE of: rxn02975.seq check: 5313 from: 1 to: 249
 VIVTNDLEVRVGARTLLDAPGQLLRVQPGDRIGLVGRNGAGKTTTMRILSGETKPYGGSV
 TTSGEIGYLPQDSREGNIEQTAR

>RXN02994 TRANSLATE of: rxn02994.seq check: 4127 from: 1 to: 723
 IKMTGVQKYFGDFHALTDIDLEIPRGQVVVVLGSPSGSKSTLCRTINRLETIEEGTIEID
 GKVLPEEGKGLANLRADVGMVFQSFNLFPHLTIKDNVTLAPIKVRKMKKSEAEKLAMSL
 ERVGIANQADKYPAQLSGGQQQVVAIARALAMNPKIMLFDEPTSAIDPEMVNEVLDMAS
 LAKEGTMVCVTHEMGFARKAADRVLFMADGLIVEDTEPDSFFTNPKSDRAKDFLGKILA
 H

>RXN03020 TRANSLATE of: rxn03020.seq check: 1931 from: 1 to: 603
 MTLHVSNNLNTVADGSTSRTLLNNIHFWMNSQAKSSVSPAHPAPENPPYSPSSAASKAPD
 SGTATLGDIDLLNPQNRAALRRNHLGIVFQQPNLLPSLTVLDDQLLLIPRLGRILPPSRSA
 RTQHKDKALSLNLSIGLGLDAKRKVSLESGGQQARVNLARALMNSPKLLLVDEPTAALDQ
 HSASEVTELIVSMAHQYNAPT

>RXN03080 TRANSLATE of: rxn03080.seq check: 3725 from: 1 to: 780
 MPQLVEIRDNLNVEFPSPRHAVKNVSFSAPAGKVTALIGPNGAGKSTALSAIAGLVESTGEV
 MVGGSGVASKAKARARLLSLVPQNTLRLIGFSARDVVAMGRYPHRRGFAVETDADRRAT
 DDALRAINALDIAEQPVNELSGGQQQLIHIGRALAQDTAVVLLDEPVSAIDLRHQVEVLQ
 LLRARANSGETTVIVVLHDLNHNHVARWCDHAVLMADGEVVSQGDIREVLEPATLSTVYGLPI
 AVRDDPETSSLRVIPHNP

>RXN03081 TRANSLATE of: rxn03081.seq check: 3848 from: 1 to: 459
 MKKSLIAIVASALVLSGCTSDSSDSSGTSGTVETTSITTSVAAADGAFPRVTLDSSIT
 LESKPERIAVLTPEAASLVLPITGADRVVMTAEMDTADEETAALASQVEYQVKNGGRLLP
 EQVVAGDPLVIVSARFDTEQGTIDILEGLNVP

>RXN03108 TRANSLATE of: rxn03108.seq check: 138 from: 1 to: 267
 MTKPNASVELNTITKSYGSTTIIGDTSITINDGEFVSLDPSGCGKSTILKMIAGLASPS
 TGTVSAGNEEIKGPGPDRGMVFQDHALLP

>RXN03116 TRANSLATE of: rxn03116.seq check: 7423 from: 1 to: 609
 MGEVDVEKHFAFGLKAAKQRRFFARTVALMPQNPTIPAGLSVFDYVLLGRHPHSYAPGRA
 DDEIVKRCLADLKLEHFSRGLDELSSGGERQVSLARALAEPRIVLLDEPTSAIDIGHA
 QETLELIDAIRHRLGLTVIAAMHDLTLTAQYGDVLMNNGGRKVFEGTAAEVLTAAQRIS
 IYDATVIVEVIDGRPVVIPQRSH

>RXN03129 TRANSLATE of: rxn03129.seq check: 210 from: 1 to: 1224
 MASIVFENVTRKYSPGARPAVDKLNLEIADGEFLVLVGPSPGCGKSTSLRMLAGLEPIDEG
 RLLIDGKDATELRPQDRDIAMVFQSYALYPNMTVRDNMGFALKNQKVAKEIEKRVAEAS
 RILQLDPYLDKPAALSGGQRQVRVAMGRAIVREPSVFCMDEPLSNLDAKLRVSTRAEISG
 LQRRMGVTTVYVTHDQVEAMTMGDRVAVLLGLVQVQVDTFQNLVDYPANAFVASFIGSPS
 MNLEGTIRGDKVTLGTGIQISVPDEVAEEVRNNPDRFEGRPVIVGARPEHMYLTANES
 GAVLGEVSHIDELGADSMVYVLASGVKNPNTDLLGEGIPEDMRVTVVGAEETDKARLGIR
 VERHHGLKAGDKVHVVAAPKDVHLFDGLDGRRIGASVLAHAHTVQSGH

>RXN03164 TRANSLATE of: rxn03164.seq check: 9986 from: 1 to: 870
 MIYRRVGNISGLKLPALISLGLWHNFGDDKPLSTQRSIIHRAFDGRGVTHFDLANNYGPPAGS
 AETNFRGRLREDLKSHRDELIISKAGWDMWPGPYGFGGSRKYLVSLLDQSLTRLGLDYV
 DIFYHHRPDPDTPLEETMYALRDIVASGKALYVGISSYGPDLTAEAAEFMAEEGCPLLIH
 QPSYSIINRWVEEPPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQG
 KSLSEGMLNVNNIDMVRKLNLDIAQERGQSLAQMALAWVLREQREYGAGLP

>RXS00088 TRANSLATE OF: RXS00088.seq check: 1389 from: 1 to: 876
 IEDNHGTEGISLPIEGVAATDNRAFELLDWRGVELVAAPLQLVPFTVTGYTEEGGVANLGSHREPDLEA
 LAAAQPSLIINGQRFQYYDDIIALNPDA TVVELDPRDGEPLDQELIRQAETLGEIFGEEEDA AKIVAD
 FESALERAKTAYAAISDQTVMAVNVSGGNIGYIAPSVGRTYGPIFDLVGLTPALEVGNASSDHEGDDIN
 VEAAIAANPDLLVMDRDGGTSTRNEADYVPAEQIVSDNEALANVKAVTDGYVYAPADTYTNENIITY
 TEILNGMADMFEKAAQ

>RXS00372 TRANSLATE OF: RXS00372.seq check: 2326 from: 1 to: 1077
 MSSKHPLKRTAVTVFALGASAAALVACSEPSDVTAEETTTASSSANASDAAGEKVITITVYSEPEEKV
 DEINKAFMEANPDIEVEVYRAGTGDLTARIEAEKASGSIEADVLWAADAATFETYAAQGD LAELEDVET
 SDIIEEALDAENFYVGTRIIP TVIAYNTEVVDQAE LPTSWADLTDPKYAGQLVMPDPAVSGAAAFNASV
 WKNDPALGEAWITALGENQPMIAQSNGPTSQEIAGGGHPVGIVVDYLVRDLAAAGSPIDTIYASEGSPY
 ITEPAGVFADSEKKEAAERYINFLLSVEGQEI AVEQAYLPVREDVGTPEGTPELADIELMTPDLEV VTA
 DKAAAVEFFQNAMN

>RXS00453 TRANSLATE OF: RXS00453.seq check: 3260 from: 1 to: 2349
 VISAWLLILAI VGGIALTMQKGFSNSFTIEDTPSIDATVSLVENFPDQTNPVTAAGVNVVFQSP EGTTL
 DDPQMMTAMDAVV DYIEDNLPDFGGGERFGNPVEVSPALEEMVIEQMTSMGLPEETA AKDAANLAVLSE
 DKTIGYTSFNIDVEAAEYVEQKHRDVINEAMQIGEDLGVRVEAGGPAFGDPIQIETTSEIIGIGIAFIV
 LIFTFGSLIAAGLPLITAVIGVGIGALAIVLATAFTDLNNVTPVLAVMIGLAVGIDYALFILSRYRAEY
 KRMPRADAAGMAVGTAGSAVVFAGATVIIALVALI IADIGFLTAMGISAAFTVFVAVLIALTFIPALLG
 VFGGHAFKGP KIPGIGNPTPKQTWEQALNRRSKGRSWVKLVQKAPGLVAVVVLGLGALTIPAMNLQLS
 LPSDSTSNIDTTQRQSADLMAEGFGAGVNAPFLVIVDTHEVNADSTALQPLIEAQEP EEEGFEFDREQAAR
 FATYMYVTQTYNSNIDVKN AQIISVNDDFTAAQILVTPYTGPADKETPELMHVLRAQEAQIEDVTGTEL
 GTTGFTAVQLDITEQLEDAMPVYLAVVGLAIFLLILVFRSLLVPLVAGLGFLLSVGAAFGATVLVWQE
 GFGGFVNTPGPLISFMPIFLIGVTFGLAMDYQVFLVTRMREHYTHHNGKGQPGSKYTPVEQSVIEGFTQ
 GSRVVTAALIMIAVFVAFIDQPLPFIKIFGFALGAGVFFDAFFIRMGLVPASMFILMGKATWWMPKWL D
 RILPSLDIEGTALEKEWEEKQAAR

>RXS00479 TRANSLATE OF: RXS00479.seq check: 9191 from: 1 to: 2190
 MSTSITTENKKKSGPPRLMRIFLPALLILVWLVGAGVG GPYFGKVSEVSSNSQTTYLPESADATQVQEQ
 LGDFTDSESI PAIVVMVSDEPLTQQDITQLNEVVAGLSEL DIVSDEVSPAIPSEDGRAVQVFVPLNPSA
 ELTESVEKLSETLTQQTPDYVSTYVTGPAGFTADLSAAFA GIDGLLLAVALAAVLVILVIVYRSFILPI
 AVLATSLFALT VALLVWWLAKWDILL LSGQTQGILFILVIGAATDYSLLYVARFREELRVQQDKGIAT
 GKAIRASVEPILASGSTVIAGLLCLLFSDLKSNSTLGPVASVGII FAMLSALTLLPALLFVFGRAFWP
 KRPKYEPEKARAKNDIPASGIWSKVADLVEQHPRAIWVSTLIVLLLGA AFVPTLKADGV SQSDLVLGSS
 EARDGQQALGEHFPGGSGSPAYII VDETQAAQAADV LNNDNFETVTVT SADSPSGSAPI TADGIVPLG
 SGTAPGPVVVEGQVLLQATLVEAPDSEEAQKAIRSIRQTFADENISAVVGGVTATSVDTNDASIHDRNL
 IIPIVLLVILVILMLLLRSIVAPLLLVTTVVSFATALGVAALLFNHVF SFGADPAVPLYGFVFLVAL
 GIDYNIFLVTRIREETKTHGTRLGILRGLTVTGGVITSAGVVLAA TFAALYVIPILFLAQIAFIVAFGV
 LIDTLLVRAFLVPALFYDIGPKIWWPSKLSNQKYQKQPQL

>RXS00654 TRANSLATE OF: RXS00654.seq check: 6625 from: 1 to: 1266
 VLDILIYPVSGVMKLWHL LHNAGLDDSLAWFFSLFGLVITIRAI IAPFTWQMYKSGRTAAHIRPHRA
 ALREEYKGYDEASIRELQKRQNDLNKEYGINPLAGCVPGLIQIPIVLGLYWALLRMARPEGLENPVF

QSIGFLTPEEVESFLAGRVSNVPLPAYVSMPTQLKYLSTTQAEVLSFVLPLFITAAILTAINMAMSMY
RSFQTN DYASGFSNGMLKFMIVMSILAPIFPLSLGLTGFPFTAIALYVWSNNLWTLTQTIIMMVILERK
YPLTDDDFKVHHELRDIYRAKQKEKRIFLWTRRKNRMLITPWNASTLHATNVELTKTRTAEINEAKQ
ARKEIANKRRETQREMNRAMQRLKQRRAEVKAKKKGLIDASPNETPSENEETKLSSPQVEPTTTAE
NREPSQED

>RXS00758 TRANSLATE OF: RXS00758.seq check: 161 from: 1 to: 1602
MTLKKS LAVTTAAALALS AACSSDSSSSSSSSSSSGEGDNYVLVNGTEPQNPLVPGNTNEVGGGRIV
DSIFSGLVYYDVGSPVNDVAESIELEGDKTYRITIKDGQTFDTGTPVTAESFVNAWNNYNVANSTLSSY
FFESILGYEEGVESMEGLQVDDTTFTVELTQPESDPFLRLGYSAFFPLPESAFDDMDAFGENPIGNP
YKLQEWNNHNDATIVPNADYTGGROAQNNDGVKFIFYPTFDSAYADLLSDNLDVLDALPDSAFSSFEDEL
SGRSINQPSAVFQSFTIPESLEHFSGEEGVLRQAISLAVNRDEITQTIFEGTRTPATDFTSPVIDGHS
DSLQADVLTYDPERAQELWAQADEISPSWGEFSISYNADGGHQAWVDATANSIRNTLGIDAIGNPYPD
FKSLRDDVTNRTINGAFRTGWQADYPSLGNFLGPLYGTGAGSNDGDYSNPDFAKLAEANAADVDAST
PLYNEAQEILLQDLPAIPTWYSNAVGGYSTNVNDNVEFQWNSQPAYYQITKN

>RXS00912 TRANSLATE OF: RXS00912.seq check: 8141 from: 1 to: 273
MDNTLYTAGLTIAAAFFMLS FIFTIYRIIVGPNSIDRLLGLDGTVMIQCSMATYICWTLDTTVTNFMM
VIALLGFISSVSVARFRKRDGA

>RXS00932 TRANSLATE OF: RXS00932.seq check: 6704 from: 1 to: 474
MTPQKLHRRFAALLEMGTWTLIIIGMILKYSVTDVAVTPIAGGIHGFGLCFAAITITVWINNKWTFPQG
IAGLIVSVIPWAALPFALWADKKGLVAGGWRFSDPSEKPHFTFFDKILAQLVRHPIRSILILLVIIAVVF
SILLAMGPPYDPDAIANTVD

>RXS01346 TRANSLATE OF: RXS01346.seq check: 3214 from: 1 to: 1575
MRTATKVIATVMAS TLAIGLASCSSSGTPDVNYVSVNGTEPQRGLIPGDTNENGGRVDMLYSGLVY
FDEAGVAQNDLAASIDQETDTTYKITLRDGIKFSGSDITATDFVDTWNEFVENGLLNTSFFSPIKGYE
EGVETLEGLNVVDDRTFTIELAQPDSEFTQRIGYYGFAPMPASARDDIDAFGENPVSSGPYKLEQWDHN
AELKVVA NEHYDGPRAANN DGLKYVFYAQNDAAYS DLLAGNLDVLDLIPPSAYTTYEEELSGRSINQPA
ASYLELSIRMESPNFEGQQQLRRQAISMAINREEIAEQIFAGTYTPALDFTAPVLDGWRDDLNGNDVL
TFQPDKARELWEDAEEIAPFEGELQISYNADVPNREWVD AVANSISNELDVNATGNPFPDFKSFRD TYR
TTGLDGAYRTAWFADYPSIGNFLGPNYTSGVASND AKYENPEFDQLIADAAA AASTKEETFQAYAQAQEM
LLRDLPAIPLWYPNVVGGYSESVDNVSVNWKAI PVYWAITKQ

>RXS01425 TRANSLATE OF: RXS01425.seq check: 9957 from: 1 to: 885
VLSPDSGITWALSIMFLTFTVRMVLVKPMVNTMRSQRKMQDMAPKMQAIREKYKNDQQMMEETRKLQK
EVGVNPIAGCLPMLVQIPVFLGLFHVLRFSFNRTGSGVGQLEMTVEQNANTPNYIFGVDEVQSFLRADLF
GAPLSSYITMPADAFDAFLGLDVSRLNIALVAAPMILII VVATHMNARLSVNRQEARKAAGKQQAASSD
QMAMQMOMMNKMLWFMPATILFTGFIWTIGLLVYMSNNVWTFQQRYYIFAKMDAEEAEEEEKRAAK
RTTAPKPGVKPENPKKRKK

>RXS01658 TRANSLATE OF: RXS01658.seq check: 7999 from: 1 to: 1833
DPQILSPTFTQQQLRN FYGFPDQLAMDRFEVDGKLRDFVVAARELDENALQQNQDWINRHTVYTHGN
GFIAAQANQVDEVARDVGSTRGGYPVYTVSDLSNARAAESED AEELGIKVDEPRVYGGPLIASATDGA
DYAIVGDTGDGPVEYD TDTSSYTYEGAGGV DIGNMVN RAMFALRYQEMNMLLSDRVGS ESILFERDPR
SRVEKVAPWLTTDSKTYPTVIDGRIKWIVDGYTTLDSL PYSTRTSLTEATQDAVMPDGT PQPLITDRVG
YIRNSVKAVVDAYDGTVELYEFDTEDPVLKAWRGVFPD TVKDGSEISDELRAHLRYPEDLFKVQRDMLA
KYNVDDSGTFFTND AFWSVPGDPTAAEGRQELKQPPYVVAADPETGESSFQLITPFRGLQREYLSAHM
SASSDPV TYGEITVRVLPTDSVTQGP KQAQDAMMSSDQVAQDQTLWRGSNDLHNGNLLTLPVGGGEILY
VEPIYSQRKDQASAFPKLLRVLV FYKGQVGYAPTIAEALSQVGIDPKEAQDIEEVDGTATTPSTDETD
DTDQPATETPTAPVSEAE GIAAINDALS NLEAARDSSFE EYGRALDALDRAVDSYQSAQ

>RXS01677 TRANSLATE OF: RXS01677.seq check: 5194 from: 1 to: 744
VNQQSKKWLVP TLVVIIAVLLI AVLLMYRGNASDTAEGVSAAATSDSAAA STAASGSASGAADSD LTS
VEARDPSDPVAVGDV DAPVGLVVFSDYQC PFCAKWSDETLPQMMKHVEDGNLRIEWREVNIFGEPSERG
ARAAYAAGLQDAYLEYHNALFANGEKPS EDLLSEEGLIKLAGDLGLDESKFTADFQSPETA VIAIAQHQQ
LGIDL GAYSTPAFL LGGQPI MGAQPASVF EAAFEQALAAKE

>RXS02586 TRANSLATE OF: RXS02586.seq check: 4914 from: 1 to: 270

MHLLRDDNWWAPGFVKKAYTVMGHGSEVEEAPRPTTTRRLNDDEEVTVEHAVVAGDTVASRGGLSTQENR
DLVSFVELKARLEKRRLLEDLD

>RXS02587 TRANSLATE OF: RXS02587.seq check: 637 from: 1 to: 2091
VFSKWGHFAYRFRRIVPLVVIAAILALFVIFGTKLGDMSQEGWDDPGSSSTAAARIELETFGRDNDGD
VVLLFTAPEGTSFDDAEVFSSISGYLDGLIENNPDEVSHINSYFDTRNQNLSSKDGTTFAALGLKGDG
EQTLKDFREIEDQLHPDNLAGGVTEVAGATAVADALDEGMAGDISRAEVFALPFVAILLLIVFGSVVA
AAMPLIVGILSILGSLGILAILAGFFQVNVFAQSVVTLGLGLAIDYGLFMVSRFREEMDKGTPVEQAV
ATTTATAGKTVVVFSAMVAVALSGLFVFPQAFLKSVAFGAISAVGLAALMSVTVLPSLFSMLGKNIDKW
SLRRTARTARRLEDTIWYRVPAMWRHAKAVTVGVVLLLLLALTVPPLTGKFGGINETYLPANDTRVAQ
ERFDEAFPAFRTEPVKLVVTGADNNQLIDIYVQANEVEGLTDRETAGATDDGTTVLSTGIQDRSLNEQ
VVEQLRAISVPEGVEVQIGGTPAMEIESIEALFEKLLWMALYIVLATFILMALVFGSVILPAKAIIMTI
LGMGATLGLITLTMFVDGVGASALNFSPGPLMSPVLVLMALIIYGLSTDYEVFLVSRMVEARDKGESTDD
AIRYGTHTGSIITAAALIMIVVCGAFGFSEIVMMKYIAFGMIAALILDATIIIRMLLVPRRDAPASRRQ
LVGTRLR

>RXS02590 TRANSLATE OF: RXS02590.seq check: 3473 from: 1 to: 936
MGISLLSSLLKIHGFPVVADFFFALAVVVAIVIIIGGWLIYRSPSFKTEVMPAWAMLSMGLIALGTASPV
VLGDDLWGFMFVCWSIGTAVGLVAYSLEYITAILRSKAGTPTFAWGLPLVTPMVASTSAAQLHEHFELPA
MLWVSFGLFLLTLASAPAVFTRVYFYFYGPKAQGIPLMATPTSWIPLGMVGQSTAAQLIGASFGSKTA
ITMGIIYGIIMGIFTIPLGAIAHFVYFRAVFKGATYSPTWWASTFPVGTLSLGAHFLSQSTGVEWFNYF
SLYLIALMLFHVIVSTIAGTIAVMRRIVGKLKSQLA

>RXS02932 TRANSLATE OF: RXS02932.seq check: 938 from: 1 to: 972
VSKTEEGRSAAIIIIYAFPTFILLGAIIFAFIFPEPFIPLTNYINIFLTIMFTMGLTLTVPDFQMVLKRP
LPILIGVVAQFVIMPFLAIVVAKMFNLNPALAVGLLMLGSGVPGGTSSNVIAFLARGDVALSVTMTSVST
IVSPIMTPFLMLLAGTETAVDGGGMAWTLVQTVLLPVIIGLVLRVFLNKWIDKILPILPYLSILGIGG
VVFAGAVAANAERLVSGLIVFVAVIVHNVLGYYVGYLTGRVFKFPEAANRTMAIEIGTQSAGLASGMAG
RFFTPEAALPGAVAALVHNITGAVYVGLVRNRPLTKASRKKESSVAVSS

>RXS03042 TRANSLATE OF: RXS03042.seq check: 1569 from: 1 to: 606
LVLAFLVLLLVERSIWVPLIAALGFGLSVLATFGATVAIFQEGAFGIIDDPQPLLSFLPIMLIGLVFGL
AMDYQIFLVTRMREGFTKGKTAGNATSNGFKHGARVVTAAALIMVSVFAAFIAQDMAFIKTMGFALAVA
VFFDAFVVRMMIIPATMFLDDKAWWLPKWLDKILPNVDVEGEGLSELHEARTEELKENVGVA

>RXS03075 TRANSLATE OF: RXS03075.seq check: 8649 from: 1 to: 726
VAKFLYKLGSTAYQKKWPFLAVWLVLIGITTLAGLYAKPTSSSFSIPGLDSVTTMEKMQERFPGSDDA
TSAPTGSVVIQAPGKTLTDPEVGAEVNQMLDEVTRATGVLKDADSVDVFLAAQGVAAQMTPALEAQGV
PAEKIAADIESISPLSADETTGIIISMTFDADSAMDISAEDREKVTNILDEYDDGDLTVVYNGNVFGAA
TSLDMTSELIGLLVAAVVLIVTFGSFIAAGMPLIS

>RXS03124 TRANSLATE OF: RXS03124.seq check: 3878 from: 1 to: 960
MTPTLASMIGLAVGIDYALFIVSRFRNELISQTGANDLEPKELAERLRTMPLAARAHAMGMAVGTAGSA
VVFAGTTVLIALVALSIINIPFLTVMAIAAAITVAIAVLVALSFLPALGLLGTTRIFAARVPGPKVPDP
EDEKPTMGLKWVRLVRKMPVAYLLVGVVLLGAIAPATNMRLAMPTDGTSTLGTAPRTGYDMTADAFGP
GRNAPMIALIDATDVPEERPLVFGQAVEQFLNTDGVKNAQITOTTENFDTAQILLPQNLMSMSAPLR
LSQLFVQMLRPSLMTPARRMALLASPFQFTMTSLLASATSWFLTF

>RXS03125 TRANSLATE OF: RXS03125.seq check: 4701 from: 1 to: 171
LVLAFLVLLLVERSIWVPLIAALGFGLSVLATFGATVAIFQEGAFGIIDDPQPLLCF

>RXS03220 TRANSLATE OF: RXS03220.seq check: 3878 from: 1 to: 960
MGLREILSSKWLVRILLVGIGLVAQQLTGINSIMYYGVVVLIEAGFSENAALIANVAPGVIAVVGAFI
ALWMDGINRRTTLITGYSLTTISHVLIGIASVAFVPGDPLRPYVILTLVVVFVGSMTFLNVATWVML
SELFPLAMRGFAIGISVFFLWIANAFGLFFPTIMEAVGLTGTFMFAGIGVVALIFIYTQVPETRGR
LEEIDEDVTSGVIFNKDIRKGVH

>RXS03221 TRANSLATE OF: RXS03221.seq check: 3878 from: 1 to: 960
MFRDPAPPSKGTTLNLGDKMASTFIQADSPEKSKLPPLTEGPYRKRLFYVALVATFGGLLFGYDTGVIN
GALNPMTRRELGLTAFTEGVVTSLLFGAAAGAMFFGRISDNWGRKTIISLAVAFFVGTMICVFAPSFA

